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OM protein - protein search, using sw model

Run on: October 9, 2003, 11:39:33 : Search time 37 Seconds  
(without alignments)  
1813.343 Million cell updates/sec

Title: US-09-687-609a-1  
Perfect score: 1371  
Sequence: 1 GSHMEGVECPFLNVLAE.....SVQPKILSGKVPYFFHQ 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP virus:\*  
16: SP bacteriophage:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349.5	96.4	896	6	O9GK17 sus scrofa
2	1346.5	96.2	912	6	O8MIKO croatica cro
3	1336.5	97.5	906	4	O9UN21 homo sapien
4	1330	97.0	730	4	O13771 homo sapien
5	1326.5	96.8	895	6	O9GKN9 sus scrofa
6	1285	93.7	333	13	O8TH77 poephila gu
7	1224	88.3	790	13	P70048 xenopus lae
8	1217	88.8	344	13	O91445 serinus can
9	1061.5	77.4	303	6	O97684 ovis aries
10	935	68.2	853	13	O93245 oncorhynch
11	930	67.8	839	13	O8OFV2 carassius a
12	928	67.7	769	13	O93497 pagrus majo
13	925	67.5	797	13	O9PM65 anguilla ja
14	911	66.4	563	13	O9DD44 halichoeres
15	909	66.3	848	13	O9YGV9 anguilla ja
16	909	66.3	854	13	O93244 oncorhynch

17	896	65.4	763	13	O8OFV7	O8qf7 haplochromi
18	884	64.5	763	13	O8UWB7	O8uwb7 oreochromis
19	797	58.1	688	13	O8UWB8	O8uwb8 oreochromis
20	792	57.8	232	13	O91A30	O91a30 anolis caro
21	782	57.0	692	13	O9W6F4	O9w6f4 haplochromi
22	774	56.5	703	13	O8UYV3	O8uyv3 xenopus lae
23	773	56.4	732	13	O9DDU9	O9ddu9 xenopus lae
24	768	56.0	583	13	O9DRV4	O9drv4 xenopus lae
25	766	55.9	939	6	O9GLM0	O9glw0 canis faml
26	759	55.4	698	11	O8BW69	O8bw69 mus musculu
27	759	55.4	711	13	O8AY12	O8ay12 rana dybows
28	734	53.5	710	13	O91BD5	O91bd5 anguilla ja
29	720	52.5	360	13	O42274	O42274 crocodylus
30	720	52.5	438	13	O90ZM7	O90zm7 petromyzon
31	711	51.9	348	13	O91425	O91425 chemidophor
32	678	49.5	401	13	O90ZM6	O90zm6 petromyzon
33	677.5	49.4	359	13	O91AC6	O91ac6 oncorhynch
34	673	49.1	298	6	O28547	O28547 ovis aries
35	668	48.7	993	13	O8JTB9	O8jtb9 haplochromi
36	664.5	48.5	779	13	O8JTB2	O8jtb2 haplochromi
37	662	48.3	689	13	O8QKX5	O8qkx5 anguilla ja
38	662	48.3	982	6	O9N0W8	O9n0w8 salmilti sci
39	658.5	48.0	793	13	O8JTB1	O8jtb1 haplochromi
40	658.5	48.0	802	13	O8JTB0	O8jtb0 haplochromi
41	654.5	47.7	793	11	O8R5J0	O8r5j0 rattus norv
42	654.5	47.7	794	11	O8R463	O8r463 rattus norv
43	628	45.8	284	13	O90Y00	O90y00 petromyzon
44	596	43.5	831	4	O8TDS3	O8tds3 homo sapien
45	590	43.0	258	6	O9BDJ7	O9bdj7 ovis aries

#### ALIGNMENTS

RESULT 1  
O9GK17  
ID O9GK17 PRELIMINARY, PRT, 896 AA.  
AC O9GK17  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Androgen receptor.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TextID=9623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Plutitary;  
RA Song J.H., Fahrenkrug S.C., Rohrer G.A., Wise T.H., Ford J.J.;  
RT "Sus scrofa androgen receptor (AR) coding sequence."  
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Plutitary;  
RA Song J.H., Fahrenkrug S.C., Rohrer G.A., Wise T.H., Ford J.J.;  
RT "Sus scrofa androgen receptor (AR) CDNA cloning: Expression in pituitary associates with FSH secretion in boars."  
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
DR EMBL, AF022775; AAC37994.1; -  
DR HSSP, P06361; IGDC.  
DR InterPro, IPR001103; Andrgn\_receptor.  
DR InterPro, IPR000536; Hormone\_rec\_1lg.  
DR InterPro, IPR001628; Znf\_C4steroid.  
DR Pfam, PF02166; Androgen\_recep. 1.  
DR Pfam, PF00104; hormone\_rec. 1.  
DR Pfam, PF00105; zfc-C4. 1.  
DR PRINTS, PR00047; STROIDPINGER.  
DR PRODOM, PD000035; Znf\_C4steroid. 1.  
DR SMART, SM00430; HOL1; 1.  
DR SMART, SM00399; Znf\_C4. 1.

DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 SQ SEQUENCE 896 AA; 97094 MW; 440F5F6E73BDC796 CRC64;

Query Match 98.4%; Score 1349.5; DB 6; Length 896;  
 Best Local Similarity 99.6%; Pred. No. 3.5e-119;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGYECOPILFVNLVLAIEIPGVVCAAGHNNQDPSPALLSSINELGERQLVHVYKAK 61  
 DB SH-IBGYECOPILFVNLVLAIEIPGVVCAAGHNNQDPSPALLSSINELGERQLVHVYKAK 697  
 QY 62 ALPGFNNLHVDDQAVIYQSWGMLVFPAMGWSFTNVSRMLYFAPDLVFNERYMHSRM 121  
 DB 698 ALPGFNNLHVDDQAVIYQSWGMLVFPAMGWSFTNVSRMLYFAPDLVFNERYMHSRM 757  
 QY 122 YSQCYRMHLSQERFGLQITPOEFLCKALLFSIIPVGLKNQKFPDELNNYIKELDR 181  
 DB 758 YSQCYRMHLSQERFGLQITPOEFLCKALLFSIIPVGLKNQKFPDELNNYIKELDR 817  
 QY 182 IIAKCKKPTSCSRFFYQLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMAAIIIS 241  
 DB 818 IIAKCKKPTSCSRFFYQLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMAAIIIS 877  
 QY 242 VQVPKILSGKVKPIYFHTQ 260  
 DB 878 VQVPKILSGKVKPIYFHTQ 896

## RESULT 2

Q8MIKO PRELIMINARY; PRT; 912 AA.

AC 08MIKO; 01-OCT-2002 (T-EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE Androgen receptor.  
 OS Crocota crocuta (Spotted hyena).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Hyenidae; Crocuta.  
 NCBI\_TaxId=9676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Catalano S., Avila D.M., McPhaul M.J., Marsico S., Wilson J.D.,  
 RA Glickman S.E.;  
 RT "Absence of association of the virilization of the female spotted  
 RT hyena with alterations of the amino acid sequence of the androgen  
 RT receptor (AR).";  
 RL Mol. Cell. Endocrinol. 0:0-0(2002).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL: AY128705; AAM96904.1; -  
 DR InterPro: IPR001103; Andrgn\_recep.  
 DR InterPro: IPR000536; Hormone\_rec\_119.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF02166; Androgen\_recep. 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR PRODOM: PD000035; Znf\_C4steroid; 1.  
 DR SMART: SM00430; HOL1; 1.  
 DR SMART: SM00399; Znf\_C4; 1.  
 DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 912 AA; 99957 MW; 8F5E35B1F743C1 CRC64;

Query Match 98.2%; Score 1346.5; DB 6; Length 912;  
 Best Local Similarity 99.2%; Pred. No. 6.8e-119;  
 Matches 257; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

2 SHMIEGYECOPILFVNLVLAIEIPGVVCAAGHNNQDPSPALLSSINELGERQLVHVYKAK 61

DB 655 SH-IBGYECOPILFVNLVLAIEIPGVVCAAGHNNQDPSPALLSSINELGERQLVHVYKAK 713  
 QY 62 ALPGFNNLHVDDQAVIYQSWGMLVFPAMGWSFTNVSRMLYFAPDLVFNERYMHSRM 121  
 DB 714 ALPGFNNLHVDDQAVIYQSWGMLVFPAMGWSFTNVSRMLYFAPDLVFNERYMHSRM 773  
 QY 122 YSQCYRMHLSQERFGLQITPOEFLCKALLFSIIPVGLKNQKFPDELNNYIKELDR 181  
 DB 774 YSQCYRMHLSQERFGLQITPOEFLCKALLFSIIPVGLKNQKFPDELNNYIKELDR 833  
 QY 182 IIAKCKKPTSCSRFFYQLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMAAIIIS 241  
 DB 834 IIAKCKKPTSCSRFFYQLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMAAIIIS 893  
 QY 242 VQVPKILSGKVKPIYFHTQ 260  
 DB 894 VQVPKILSGKVKPIYFHTQ 912

## RESULT 3

Q9UN21 PRELIMINARY; PRT; 906 AA.

AC 09UN21; 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)  
 DE Androgen receptor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Breast carcinoma;  
 RA Jin C.H., Urcan-Bisiel M.S., Schrader W.T.;  
 RT "Androgen receptor sequences in human mammary carcinoma MDA-MB-453  
 RT cells.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL: AF162704; AAD45921.1; -  
 DR HSRP: P06536; IGDC.  
 DR InterPro: IPR001103; Andrgn\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec\_119.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF02166; Androgen\_recep. 1.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR PRODOM: PD000035; Znf\_C4steroid; 1.  
 DR SMART: SM00430; HOL1; 1.  
 DR SMART: SM00399; Znf\_C4; 1.  
 DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 906 AA; 97884 MW; 0A1FA802B2BDAD CRC64;

Query Match 97.5%; Score 1336.5; DB 4; Length 906;  
 Best Local Similarity 98.5%; Pred. No. 6e-118;  
 Matches 255; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 SHMIEGYECOPILFVNLVLAIEIPGVVCAAGHNNQDPSPALLSSINELGERQLVHVYKAK 61  
 DB 649 SH-IBGYECOPILFVNLVLAIEIPGVVCAAGHNNQDPSPALLSSINELGERQLVHVYKAK 707  
 QY 62 ALPGFNNLHVDDQAVIYQSWGMLVFPAMGWSFTNVSRMLYFAPDLVFNERYMHSRM 121  
 DB 708 ALPGFNNLHVDDQAVIYQSWGMLVFPAMGWSFTNVSRMLYFAPDLVFNERYMHSRM 767  
 QY 122 YSQCYRMHLSQERFGLQITPOEFLCKALLFSIIPVGLKNQKFPDELNNYIKELDR 181  
 DB 768 YSQCYRMHLSQERFGLQITPOEFLCKALLFSIIPVGLKNQKFPDELNNYIKELDR 827

QY 182 IIAKCKNPTSCRRFYOLTKLDSVOPILARELHOFTFDLLIKSHVSVDPPEMAEITIS 241  
 DB 828 IIAKCKNPTSCRRFYOLTKLDSVOPILARELHOFTFDLLIKSHVSVDPPEMAEITIS 887  
 QY 242 VQVPKILSGKVPKIPYFHTQ 260  
 DB 888 VQVPKILSGKVPKIPYFHTQ 906

## RESULT 4

Q13771 PRELIMINARY; PRT; 730 AA.  
 AC Q13771;  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Androgen receptor.  
 GN AR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=90258935; PubMed=2342476;  
 RA Govindan M.V.;  
 RT "Specific region in hormone binding domain is essential for hormone  
 RT binding and trans-activation by human androgen receptor."  
 RL Mol. Endocrinol. 4:417-427(1990).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL: W73069; AAA51735.1; --  
 DR HSSP: P06536; IGDC.  
 DR InterPro: IPR001103; Andrgn\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec.1g.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF02166; Androgen\_recep. 1.  
 DR Pfam: PF00104; hormone\_rec. 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid. 1.  
 DR SMART: SM00430; HOL1. 1.  
 DR SMART: SM00399; Znf\_C4; 1.  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.  
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 730 AA; 79150 MW; 918847C3B41B80C9 CRC64;

Query Match 97.0%; Score 1330; DB 4; Length 730;  
 Best Local Similarity 96.6%; Pred. No. 1.9e-117;  
 Matches 257; Conservative 0; Mismatches 1; Indels 8; Gaps 2;

QY 2 SHMIEGYECOPITFLNVLAIIEPGVVCAGHDNNQPDSPFALLSLINELGERQLVHVYKMAK 61  
 DB 466 SH-IEGYECOPITFLNVLAIIEPGVVCAGHDNNQPDSPFALLSLINELGERQLVHVYKMAK 524  
 QY 62 ALPGFRLNHLVDQMAVIQYSWMGLVWFAMGWSFTVNSRMLYFAPDLVFNERYMKSRM 121  
 DB 525 ALPGFRLNHLVDQMAVIQYSWMGLVWFAMGWSFTVNSRMLYFAPDLVFNERYMKSRM 584  
 QY 122 YSQCYRMHLSQERFQMLITPQEFCKKALLFSIIPVGLGNQKFPDELRLN 174  
 DB 585 YSQCYRMHLSQERFQMLITPQEFCKKALLFSIIPVGLGNQKFPDELRLN 644  
 QY 175 YIKELDRILIAKCKNPTSCRRFYOLTKLDSVOPILARELHOFTFDLLIKSHVSVDPPE 234  
 DB 645 YIKELDRILIAKCKNPTSCRRFYOLTKLDSVOPILARELHOFTFDLLIKSHVSVDPPE 704  
 QY 235 MMAEITISVQVPKILSGKVPKIPYFHTQ 260  
 DB 705 MMAEITISVQVPKILSGKVPKIPYFHTQ 730

## RESULT 5

ID 09GKN9 PRELIMINARY; PRT; 895 AA.  
 AC 09GKN9;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Androgen receptor AR.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_Taxid=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20539123; PubMed=11086548;  
 RA Trakooljul N., Ponsuksili S., Scheilander K., Wimmers K.;  
 RT "A highly polymorphic repetitive polypyrimidine/polypurine (CCTTT)<sub>n</sub>  
 RT sequence in the 5' untranslated sequence of the porcine androgen  
 RT receptor gene."  
 RL Anim. Genet. 31:288-289(2000).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL: AF161717; AAG40566.1; --  
 DR HSSP: P06536; IGDC.  
 DR InterPro: IPR001103; Andrgn\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec.1g.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF02166; Androgen\_recep. 1.  
 DR Pfam: PF00104; hormone\_rec. 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid. 1.  
 DR SMART: SM00430; HOL1. 1.  
 DR SMART: SM00399; Znf\_C4; 1.  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.  
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 895 AA; 97156 MW; 923C2FDD1F7E4779 CRC64;

Query Match 96.8%; Score 1326.5; DB 6; Length 895;  
 Best Local Similarity 98.1%; Pred. No. 5.2e-117;  
 Matches 254; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 SHMIEGYECOPITFLNVLAIIEPGVVCAGHDNNQPDSPFALLSLINELGERQLVHVYKMAK 61  
 DB 638 SH-IEGYECOPITFLNVLAIIEPGVVCAGHDNNQPDSPFALLSLINELGERQLVHVYKMAK 696  
 QY 62 ALPGFRLNHLVDQMAVIQYSWMGLVWFAMGWSFTVNSRMLYFAPDLVFNERYMKSRM 121  
 DB 697 ALPGFRLNHLVDQMAVIQYSWMGLVWFAMGWSFTVNSRMLYFAPDLVFNERYMKSRM 756  
 QY 122 YSQCYRMHLSQERFQMLITPQEFCKKALLFSIIPVGLGNQKFPDELRLN 181  
 DB 757 YSQCYRMHLSQERFQMLITPQEFCKKALLFSIIPVGLGNQKFPDELRLN 816  
 QY 182 IIAKCKNPTSCRRFYOLTKLDSVOPILARELHOFTFDLLIKSHVSVDPPEMAEITIS 241  
 DB 817 IIAKCKNPTSCRRFYOLTKLDSVOPILARELHOFTFDLLIKSHVSVDPPEMAEITIS 876  
 QY 242 VQVPKILSGKVPKIPYFHTQ 260  
 DB 877 VQVPKILSGKVPKIPYFHTQ 895

## RESULT 6

ID 08JH77 PRELIMINARY; PRT; 333 AA.  
 AC 08JH77;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DR Androgen receptor (Fragment).  
 OS Poephila guttata (Zebra Finch) (Taeniopygia guttata).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;  
 OC Estrildinae; Taeniopygia.  
 NCBI\_TaxID=59729;  
 OX  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Perlman W.R., Ramachandran B., Arnold A.P.;  
 RT "Expression of Androgen Receptor mRNA in the Late Embryonic and Early  
 RT Post-hatch Zebra Finch Brain."  
 RL Submitted (Jun-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL; AF532914; AAM9669.1; -.  
 DR InterPro; IPR000536; Hormone\_rec\_1lg.  
 DR InterPro; IPR001723; Steroidm\_receptor.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00398; STRDHOMONER.  
 DR ProDom; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; ZNF\_C4; 1.  
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 FT NON\_TER  
 SQ SEQUENCE 333 AA; 38536 MW; B36A778B710B790 CRC64;  
 Query Match 93.7%; Score 1285; DB 113; Length 333;  
 Best Local Similarity 93.4%; Pred. No. 1.4e-113;  
 Matches 229; Conservative 12; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 IEGYECOPIFLNVLAIEPGVVCAGHNNQPDSPFALLSSINELGERQLVHVVKAKALP 64  
 DB 78 IGYECOPIFLNVLAIEPGVVCAGHNNQPDSPFALLSSINELGERQLVHVVKAKALP 137  
 QY 65 GRRNLAVDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNRYRMRKSR 124  
 DB 138 GRRNLAVDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNRYRMRKSR 197  
 QY 125 CVRMRLHLSOERGMQITPQELCKALLPSIIPVGLKNKCFDELRMNYIKELDRITA 184  
 DB 198 CIRMRLHLSOERGMQITPQELCKALLPSIIPVGLKNKCFDELRMNYIKELDRITA 257  
 QY 185 CRRKNPTSCSRPFYQITKLDVQPIARELHOFPTDLIKSHMVSVDPEMMAEIIISGV 244  
 DB 258 CRRKNPTSCSRPFYQITKLDVQPIARELHOFPTDLIKSHMVSVDPEMMAEIIISGV 317  
 QY 245 PKILSGKVPDYPHNQ 260  
 DB 318 PKILSGKVPDYPHNQ 333  
 RESULT 7  
 P70048 PRELIMINARY; PRT; 790 AA.  
 AC P70048;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Androgen receptor alpha isoform.  
 GN XL ALPHA.AR.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93376782; PubMed=7690145;  
 RA Fischer L., Catz D., Kelley D.;  
 RT "An androgen receptor mRNA isoform associated with hormone-induced

RT cell proliferation.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 90:8254-8258(1993).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95324753; PubMed=7601302;  
 RA Fischer L.M., Catz D., Kelley D.B.;  
 RT "Androgen-directed development of the Xenopus laevis larynx: control  
 RT of androgen receptor expression and tissue differentiation.";  
 RL Dev. Biol. 170:115-126(1995).  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Kelley D.B., Kamenetz F.R., Kelley D.B., Badae T.C.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL; U67129; AAC97386.1; -.  
 DR HSP; P06536; IGDC.  
 DR InterPro; IPR001103; Andrgn\_receptor.  
 DR InterPro; IPR000536; Hormone\_rec\_1lg.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF02166; Androgen\_recip; 1.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR PRINTS; PR00047; STROIDPINGER.  
 DR ProDom; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; ZNF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 790 AA; 86973 MW; 9E7FCL36CCCG3906 CRC64;  
 Query Match 89.3%; Score 1224; DB 113; Length 790;  
 Best Local Similarity 88.4%; Pred. No. 2.4e-107;  
 Matches 228; Conservative 15; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 GSHMIEGYECOPIFLNVLAIEPGVVCAGHNNQPDSPFALLSSINELGERQLVHVVKMA 60  
 DB 531 GIPQIEGYECOPIFLNVLAIEPGVVCAGHNNQPDSPFALLSSINELGERQLVHVVKMA 590  
 QY 61 KALPGFRNLAVDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNRYRMRKSR 120  
 DB 591 KALPGFRNLAVDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNRYRMRKSR 650  
 QY 121 MYSQCVRRRLHLSOERGMQITPQELCKALLPSIIPVGLKNKCFDELRMNYIKELD 180  
 DB 651 MYSQCVRRRLHLSOERGMQITPQELCKALLPSIIPVGLKNKCFDELRMNYIKELD 710  
 QY 181 RIACKRKNPTSCSRPFYQITKLDVQPIARELHOFPTDLIKSHMVSVDPEMMAEII 240  
 DB 711 RIACKRKNPTSCSRPFYQITKLDVQPIARELHOFPTDLIKSHMVSVDPEMMAEII 770  
 QY 241 SVQVPEKILSGKVPDYPH 258  
 DB 771 SVQVPEKILSGKVPDYPH 788  
 RESULT 8  
 Q91445 PRELIMINARY; PRT; 344 AA.  
 AC Q91445;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Androgen receptor (Fragment).  
 GN AR.  
 OS Serinus canaria (Canary).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeridae;  
 OC Fringillidae; Carduelinae; Serinus.  
 OX NCBI\_TaxID=9135;  
 RN  
 RP SEQUENCE FROM N.A.

RC TISSUE=Testis; PubMed=8299561;  
 RX MEDLINE=94130808; Clayton D.F.;  
 RA Nastiuk K.L.; Clayton D.F.;  
 RT "Seasonal and tissue-specific regulation of canary androgen receptor  
 RT messenger ribonucleic acid";  
 RL Endocrinology 134:640-649(1994).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC EMBL, L25901; AAA17402.1; -.  
 DR HSP, P06536; 1GU.  
 DR InterPro: IPR000536; Hormone\_rec\_11g.  
 DR InterPro: IPR001723; Steroid\_receptor.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00398; STRDHOMONER.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid; 1.  
 DR SMART: SM00430; HOL1; 1.  
 DR SMART: SM00399; Znf\_C4; 1.  
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT SEQUENCE 344 AA; 39376 MW; 713676394FC0B030 CRC64;

Query Match  
 Best Local Similarity 92.7%; Score 1217; DB 13; Length 344;  
 Matches 227; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY 5 IEGYECOPIFLVNLAIEPGVYAGHDNNOPOSPFALLSLNIEGROLVHVYKAKALP 64  
 Db 100 IEGYECOPIFLVNLAIEPGVYAGHDNNOPOSPFALLSLNIEGROLVHVYKAKALP 159  
 QY 65 GRRNLHVDQMAVIOYSNMGMLVFMGWSFTVNSRMLYFAPDLVFNERYHKSMSQ 124  
 Db 160 GRRNLHVDQMAVIOYSNMGMLVFMGWSFTVNSRMLYFAPDLVFNERYHKSMSQ 219  
 QY 125 CVRMHLSQEFQWLOITPOEFLCKMALLFSIIPVGLKNOKFPDELNNYTKELDRITA 184  
 Db 220 CTRMHLSEBFQWLOITPOEFLCKMALLFSIIPVGLKNOKFPDELNNYTKELDRITA 279  
 QY 185 CRRKPTSCSRPFYQITKLDSVQPIARELHOFTDILLKSHVSVDPENMAEIIISVQV 244  
 Db 280 CRRKPTSCSRPFYQITKLDSVQPIARELHOFTDILLKSHVSVDPENMAEIIISVQV 339  
 QY 245 PKILS 249  
 Db 340 PKILS 344

RESULT 9  
 097684 PRELIMINARY; PRT; 303 AA.

ID 097684  
 AC 097684;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Androgen receptor (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dorset;  
 RA "Thomney M.L., Ignatz G., Richards H.M.;  
 RA "Partial sequence of an ovine androgen receptor cDNA";  
 RA Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL, AF105713; AAC97958.1; -.

DR HSP, P06536; 1GU.  
 DR InterPro: IPR000536; Hormone\_rec\_11g.  
 DR InterPro: IPR001723; Steroid\_receptor.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00398; STRDHOMONER.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid; 1.  
 DR SMART: SM00430; HOL1; 1.  
 DR SMART: SM00399; Znf\_C4; 1.  
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT SEQUENCE 303 AA; 34673 MW; D14D3950C7DC69D1 CRC64;

Query Match  
 Best Local Similarity 77.4%; Score 1061.5; DB 6; Length 303;  
 Matches 201; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGECOPIFLVNLAIEPGVYAGHDNNOPOSPFALLSLNIEGROLVHVYKAKALP 61  
 Db 103 SH-IEGYECOPIFLVNLAIEPGVYAGHDNNOPOSPFALLSLNIEGROLVHVYKAKALP 161  
 QY 62 ALPGFRNLHVDQMAVIOYSNMGMLVFMGWSFTVNSRMLYFAPDLVFNERYHKSMSQ 121  
 Db 162 ALPGFRNLHVDQMAVIOYSNMGMLVFMGWSFTVNSRMLYFAPDLVFNERYHKSMSQ 221  
 QY 122 YSQCVRMHLSEBFQWLOITPOEFLCKMALLFSIIPVGLKNOKFPDELNNYTKELDRITA 181  
 Db 222 YSQCVRMHLSEBFQWLOITPOEFLCKMALLFSIIPVGLKNOKFPDELNNYTKELDRITA 281  
 QY 182 IIAKRRKPTSCSRPFYQITKL 203  
 Db 282 IIAKRRKPTSCSRPFYQITKL 303

RESULT 10  
 093245 PRELIMINARY; PRT; 853 AA.

ID 093245  
 AC 093245;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Androgen receptor beta.  
 GN AR-BETA.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=99150354; PubMed=10026186;  
 RA Takeo J., Yamashita S.;  
 RT "Two distinct isoforms of cDNA encoding rainbow trout androgen  
 RT receptors";  
 RL J. Biol. Chem. 274:5674-5680(1999).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC EMBL, AB012096; BA32785.1; -.  
 DR HSP, P06536; 1GDC.  
 DR InterPro: IPR001103; Andrgn\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec\_11g.  
 DR InterPro: IPR001723; Steroid\_receptor.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS: PR00398; STRDHOMONER.  
 DR PRINTS: PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid; 1.

DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; ZNF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 853 AA; 95776 MW; 65EPF5FD3836P4C4 CRC64;

Query Match 68.2%; Score 935; DB 13; Length 853;  
 Best Local Similarity 70.4%; Pred. No. 6, 6e-80;  
 Matches 178; Conservative 35; Mismatches 36; Indels 4; Gaps 2;

QY 8 YECOPFLNVLTAIEPGVAGHDNNOPDSFALLSLNELGEROLVHVYKAKALPGFR 67  
 DB 602 FHSQVFLNLTLESIEPEVNAAGHDGCPDSAAVLLSLNELGEROLVHVYKAKALPGFR 661  
 QY 68 NLAHVDQMAVIOYSWGMGLVFMGMRSTNNNSMLYFAPDLVFNEXYMRKSRMSQCVR 127  
 DB 662 NLAHVDQMTVIOHVMGVMVFMGLGMSYKNNANMLYFAPDLVFNDRHMLISMVHEHCVR 721  
 QY 128 MRHLSQEFGLQITPQEFLLCKALLLSIIIPVDGLKNOKFPDELRLMYIKELDRITACKR 187  
 DB 722 MRHLSQEFVLLQVTOEFLCKALLLSIIIPVDGLKNOKFPDELRLMYIKELDRITACKR 781  
 QY 188 KNPTSCSRFYOTLTLDVQPIARELHOFTFDLTKSHV--SYDPEPMARITISVOVP 245  
 DB 782 K--TNCARFOQLRLMDSLQPIVRKLOFTFDLFOASLPTKVSPEMTAIIISVOVP 839  
 QY 246 KILSGKVPRIYFH 258  
 DB 840 KILAGLAKPILFH 852

## RESULT 11

Q8QFV2 PRELIMINARY; PRT; 839 AA.

AC Q8QFV2; 08QFV2;  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Androgen receptor.  
 GN AR.  
 OS Carassius auratus (Goldfish).  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OC NCBI\_TaxID=7957;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Betka M., Rothberg S.C., Callard G.V.;  
 RT "Carassius auratus Androgen Receptor";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL: AY090897; AA09278.1; -  
 DR InterPro: IPR001103; Andrgn\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec\_119.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF02166; Androgen\_recip. 1.  
 DR Pfam: PF00104; hormone\_rec. 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR Prodom: PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; ZNF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 839 AA; 93168 MW; A53ADC3169COBIF4 CRC64;

Query Match 67.8%; Score 930; DB 13; Length 839;  
 Best Local Similarity 70.4%; Pred. No. 1, 9e-79;  
 Matches 178; Conservative 35; Mismatches 36; Indels 4; Gaps 2;

QY 8 YECOPFLNVLTAIEPGVAGHDNNOPDSFALLSLNELGEROLVHVYKAKALPGFR 67  
 DB 588 FHSQVFLNLTLESIEPEVNAAGHDGCPDSAAVLLSLNELGEROLVHVYKAKALPGFR 647  
 QY 68 NLAHVDQMAVIOYSWGMGLVFMGMRSTNNNSMLYFAPDLVFNEXYMRKSRMSQCVR 127  
 DB 648 NLAHVDQMTVIOHVMGVMVFMGLGMSYKNNANMLYFAPDLVFNDRHMLISMVHEHCVR 707  
 QY 128 MRHLSQEFGLQITPQEFLLCKALLLSIIIPVDGLKNOKFPDELRLMYIKELDRITACKR 187  
 DB 708 MRHLSQEFVLLQVTOEFLCKALLLSIIIPVDGLKNOKFPDELRLMYIKELDRITACKR 767  
 QY 188 KNPTSCSRFYOTLTLDVQPIARELHOFTFDLTKSHV--SYDPEPMARITISVOVP 245  
 DB 768 K--TNCARFOQLRLMDSLQPIVRKLOFTFDLFOASLPTKVSPEMTAIIISVOVP 825  
 QY 246 KILSGKVPRIYFH 258  
 DB 826 KILAGLAKPILFH 838

## RESULT 12

O93497 PRELIMINARY; PRT; 769 AA.

AC O93497;  
 DT 01-NOV-1998 (TRENBLrel. 08, Created)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Androgen receptor.  
 OS Pagrus major (Red sea bream) (Chrysophrys major).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;  
 OC Sparidae; Pagrus.  
 OC NCBI\_TaxID=143350;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99326178; Pubmed-10395960;  
 RA Tounaca K., Kinoshita M., Tokuda Y., Toyohara H., Sakaguchi M.,  
 RA Yokoyama Y., Yamashita S.;  
 RT "Sequence and expression of a cDNA encoding the red seabream androgen  
 RT receptor";  
 RL Blochim. Biophys. Acta 1450:481-485(1999).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
 DR EMBL: AB017158; BA33451.1; -  
 DR HSP; P06536; IRGD.  
 DR InterPro: IPR001103; Andrgn\_receptor.  
 DR InterPro: IPR000536; Hormone\_rec\_119.  
 DR InterPro: IPR001723; Sterhnm\_receptor.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF02166; Androgen\_recip. 1.  
 DR Pfam: PF00104; hormone\_rec. 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS; PR00398; STRODHOMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR Prodom: PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; ZNF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 769 AA; 86081 MW; 9305C627DBR42062 CRC64;

Query Match 67.7%; Score 928; DB 13; Length 769;  
 Best Local Similarity 70.8%; Pred. No. 2, 7e-79;  
 Matches 179; Conservative 29; Mismatches 41; Indels 4; Gaps 2;

QY 8 YECOPFLNVLTAIEPGVAGHDNNOPDSFALLSLNELGEROLVHVYKAKALPGFR 67  
 DB 518 FHSQVFLNLTLESIEPEVNAAGHDGCPDSAAVLLSLNELGEROLVHVYKAKALPGFR 577  
 QY 68 NLAHVDQMAVIOYSWGMGLVFMGMRSTNNNSMLYFAPDLVFNEXYMRKSRMSQCVR 127

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Db 578 NLAHDDDMTAYIQSHWKMVWVFGILGMRYSKYVKNNGMLYFAPDLVYNEHRMHISTMYECIR 637
QY 128 MRHLSQEPGWLQITPOEFLCKAKALLFSIIPVDGLKNQKPEFDELKMYIKELDRACKR 187
Db 638 MRHLSQEPFLLOITQOEFLCKAKALLFSIIPVEGLSKQKFEDELKLYINELDLINRM 697
QY 188 KNPFGSGRRFYQLTKLDSVQPIARELHOFTFDLLIKSHNV--SYDPEMMAELISVQVP 245
Db 698 N--TNCQRFYQLTRLDLSQMTVKLHOFPLDFOAQLPTKVSPEMIGELISVHP 755
QY 246 KILSGKVPITYFH 258
Db 756 KILAGLAKPILFH 768

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## RESULT 13

Q9PMG5 PRELIMINARY; PRT; 797 AA.

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AC 09PMG5; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Androgen receptor-beta.
GN AR-BETA.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_Taxid=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99395076; Pubmed=10464240;
RT Ikeuchi T., Todo T., Kobayashi T., Nagahama Y.;
RT "CDNA cloning of a novel androgen receptor subtype.";
RL J. Biol. Chem. 274:25205-25205(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL; AB025361, BAA83805.1, -.
DR HSSP; P06536; 1GDC.
DR InterPro; IPR001103; Andrgn_receptor.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR001723; Sterdmn_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF02166; Androgen_recep; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDPTNGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; ZNF C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 797 AA; 89924 MW; CFIDSP21BBA5691 CRC64;

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Query Match 67.5%; Score 925; DB 13; Length 797;

Best Local Similarity 69.2%; Pred. No. 5.4e-79;

Matches 175; Conservative 35; Mismatches 39; Indels 4; Gaps 2;

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QY 8 YECQPIPLAVLAIEBPGVACAGHNNQPDSPALISLNLGEGOLVHYVYKAKALPGRR 67
Db 546 PFTQGVPLNLTLESIBPEVYVNAHDYQGDTSATLTLSNELGEGOLVHYVYKAKALPGRR 605
QY 68 NLAHDDDMTAYIQSHWKMVWVFGILGMRYSKYVKNNGMLYFAPDLVYNEHRMKSRYMSQCVR 127
Db 606 NLAHDDDMTAYIQSHWKMVWVFGILGMRYSKYVKNNGMLYFAPDLVYNEHRMKSRYMSQCVR 665
QY 128 MRHLSQEPGWLQITPOEFLCKAKALLFSIIPVDGLKNQKPEFDELKMYIKELDRACKR 187
Db 666 MRHLSQEPFLLOITQOEFLCKAKALLFSIIPVEGLSKQKFEDELKLYINELDLINRM 725

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QY 188 KNPFGSGRRFYQLTKLDSVQPIARELHOFTFDLLIKSHNV--SYDPEMMAELISVQVP 245
Db 726 K--TNCQRFYQLTRLDLSQMTVKLHOFPLDFOAQLPTKVSPEMIGELISVHP 783
QY 246 KILSGKVPITYFH 258
Db 784 KILAGLAKPILFH 796

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## RESULT 14

Q9DDJ4 PRELIMINARY; PRT; 563 AA.

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AC 09DDJ4; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Androgen receptor (Fragment).
GN AR.
OS Halichoeres trimaculatus (three-spot wrasse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Labridae; Halichoeres.
OX NCBI_Taxid=147232;
RN [1]
RP SEQUENCE FROM N.A.
RA Klm S.J., Ket O., Takemura A., Nakamura M.;
RT Partial sequence and expression of androgen and estrogen receptor
RT genes in the protogynous wrasse, Halichoeres trimaculatus.
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL; AF326200; AAG48340.1, -.
DR HSSP; P06536; 1RGD.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR001723; Sterdmn_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDPTNGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; ZNF C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON TER 1
SQ SEQUENCE 563 AA; 64352 MW; A744C3728F004A6 CRC64;

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Query Match 66.4%; Score 911; DB 13; Length 563;

Best Local Similarity 69.6%; Pred. No. 7.5e-78;

Matches 176; Conservative 31; Mismatches 42; Indels 4; Gaps 2;

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QY 8 YECQPIPLAVLAIEBPGVACAGHNNQPDSPALISLNLGEGOLVHYVYKAKALPGRR 67
Db 312 PNTQMAFLNLTLESIBPEVYVNAHDYQGDTSATLTLSNELGEGOLVHYVYKAKALPGRR 371
QY 68 NLAHDDDMTAYIQSHWKMVWVFGILGMRYSKYVKNNGMLYFAPDLVYNEHRMKSRYMSQCVR 127
Db 372 NLAHDDDMTAYIQSHWKMVWVFGILGMRYSKYVKNNGMLYFAPDLVYNEHRMKSRYMSQCVR 431
QY 128 MRHLSQEPGWLQITPOEFLCKAKALLFSIIPVDGLKNQKPEFDELKMYIKELDRACKR 187
Db 432 MRHLSQEPFLLOITQOEFLCKAKALLFSIIPVEGLSKQKFEDELKLYINELDLINRM 491
QY 188 KNPFGSGRRFYQLTKLDSVQPIARELHOFTFDLLIKSHNV--SYDPEMMAELISVQVP 245
Db 492 K--TNCQRFYQLTRLDLSQMTVKLHOFPLDFOAQLPTKVSPEMIGELISVHP 549
QY 246 KILSGKVPITYFH 258

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Db 550 KILAGLAKPILFH 562

## RESULT 15

09YGV9 PRELIMINARY; PRT; 848 AA.  
AC 09YGV9;  
DT 01-MAY-1999 (TEMBLrel. 10, Created)  
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)  
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
DE Androgen receptor alpha.  
OS Anguilla japonica (Japanese eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguilla.  
OX NCBI\_TaxID=7937;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=99119319; PubMed=9918846;  
RA Todo T., Ikeuchi T., Kobayashi T., Nagahama Y.,  
RT "Fish androgen receptor: cDNA cloning, steroid activation of  
RT transcription in transfected mammalian cells, and tissue mRNA  
RT levels."  
RL Biochem. Biophys. Res. Commun. 254:378-383(1999).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
DR EMBL; AB023960; BAA75464.1; -.  
DR HSSP; P06536; IGDC.  
DR InterPro; IPR001103; Andrgn\_receptor.  
DR InterPro; IPR000536; Hormone\_rec\_11g.  
DR InterPro; IPR001723; Sterhma\_receptor.  
DR InterPro; IPR001628; Znf\_CsteroId.  
DR Pfam; PF02166; Androgen\_recep; 1.  
DR Pfam; PF00104; hormone\_rec; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00398; STRDHOMONER.  
DR PRINTS; PR00047; STROLDPRNGER.  
DR ProDom; PD000035; Znf\_CsteroId; 1.  
DR SMART; SM00430; HOL1; 1.  
DR SMART; SM00399; ZNF\_C4; 1.  
DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;  
KW Transcription regulation; Zinc; Zinc-finger.  
SQ SEQUENCE 848 AA; 94692 MW; A8889AF7F2E50D3E CRC64;

Query Match. 66.3%; Score 909; DB 13; Length 848;  
Best Local Similarity 68.5%; Pred. No. 1,9e-77;  
Matches 174; Conservative 36; Mismatches 40; Indels 4; Gaps 2;

0Y 7 GYECPIPLNVLIAIPGVVCAQHNNQDSPAALLSSINELGERQLVHVYVWKAALPGF 66  
Db 596 GPHTSQMFNIIIEAIEPEVYVNAHGYGQPDASAASLITSLNELGERQLVHVYVWKAALPGF 655  
0Y 67 ENLHYDDQMAVVOYGMGMVAFAMGWRSTNNSRLVYAPDLVFNEXYRMHKSRYSCV 126  
Db 656 KSLVYDDQMTVIOHSMAMVAFALGSRKXKYSRLYFAPLVFNEMQVSTNTEHCT 715  
0Y 127 RNRHLSOERGMLOITPOEFLCKKALLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACK 186  
Db 716 RKNKNSQERFAMLOVQOEFLCKKALLFSITIVPEGLKGNFDELARSLINELDLVSR 775  
0Y 187 RKNPTSCRRFPQTLKLDSDVQPIARELHOFTEFLIKSHMYS--VDPEMAELISVQV 244  
Db 776 SK--SSCSERFOQLTRLDSLOPLVKLQHPTEFLVQSONLNQVCEPEMISRIISVHV 833  
0Y 245 PRLSGKVPIYFH 258  
Db 834 PKILAGTVKPILFH 847

Search completed: October 9, 2003, 11:42:15  
Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 9, 2003, 11:39:08 ; Search time 11 Seconds

(without alignments)  
1111.540 Million cell updates/sec

Title: US-09-687-609a-1  
Sequence: 1 GSHMIEGYECDFINLVLEA.....SVQVPIKISGKVKPIYFHTQ 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349.5	98.4	709	1	ANDR_RABIT
2	1349.5	98.4	884	1	ANDR_EULFC
3	1349.5	98.4	895	1	ANDR_MACFA
4	1349.5	98.4	895	1	ANDR_PAPHA
5	1349.5	98.4	899	1	ANDR_MOUSE
6	1349.5	98.4	902	1	ANDR_RAT
7	1349.5	98.4	907	1	ANDR_CANPA
8	1349.5	98.4	911	1	ANDR_PANTR
9	1349.5	98.4	919	1	ANDR_HUMAN
10	766	55.9	930	1	PRGR_RABIT
11	765	55.8	933	1	PRGR_HUMAN
12	759	55.4	923	1	PRGR_RAT
13	758	55.3	923	1	PRGR_MOUSE
14	752	55.9	786	1	PRGR_CHICK
15	738	53.8	377	1	PRGR_SHEEP
16	677.5	49.4	359	1	MCR_ONCOMY
17	666	48.6	978	1	MCR_MOUSE
18	665	48.5	984	1	MCR_HUMAN
19	664.5	48.5	777	1	GCR_AOTNA
20	664.5	48.5	777	1	GCR_SAIIB
21	664.5	48.5	778	1	GCR_SAIISC
22	662.5	48.3	777	1	GCR_HUMAN
23	662	48.3	981	1	MCR_RAT
24	662	48.3	982	1	MCR_SAIISC
25	661.5	48.2	777	1	GCR_SAIISC
26	660.5	48.2	772	1	GCR_RABIT
27	660	48.1	612	1	MCR_XENLA
28	657.5	48.0	783	1	GCR_MOUSE
29	653.5	47.6	776	1	GCR_TUPGB
30	651.5	47.5	807	1	GCR_PAROL
31	650.5	47.4	776	1	GCR_XENLA
32	648.5	47.3	758	1	GCR_ONCOMY
33	644.5	47.0	771	1	GCR_CAVPO

34	638.5	46.6	795	1	GCR_RAT	P06536	rattus norv
35	615	44.9	977	1	MCR_TUPGB	O29131	tupaia glis
36	590	43.0	258	1	MCR_SHEEP	O9bdj7	ovis aries
37	580	42.3	711	1	GCR_PIG	O9nlus	sus scrofa
38	591	28.5	164	1	MCR_PIG	P79404	sus scrofa
39	387	28.2	180	1	PRGR_MACRU	P79373	macropus eu
40	342	24.9	147	1	MCR_CHICK	O8gh12	gallus gall
41	237	17.3	569	1	ESR1_BRARE	P57717	brachydonto
42	228.5	16.7	581	1	ESR1_PAGMA	O42132	pagrus majo
43	227.5	16.6	617	1	ESR1_ICTPU	O9yhz7	ictalurus p
44	223	16.3	307	1	ESR1_CNEON	O91424	chemidophor
45	222	16.2	535	1	ESR1_SALSA	P50242	salmo salar

## ALIGNMENTS

```

RESULT 1
ANDR_RABIT
ID ANDR_RABIT
AC P49659, 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE Androgen receptor (Dihydrotestosterone receptor) (Fragment).
GN AR OR NR3C4.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Prostate;
RX MEDLINE=9604463; PubMed=7559153;
RA Krongrad A., Wilson J.D., McPhaul M.J.,
RT "Cloning and partial sequence of the rabbit androgen receptor:
RT expression in fetal urogenital tissues.",
RL J. Androl. 16:209-212(1995).
CC CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
-----
DR EMBL: U16366; AAC46469.1; -
DR HSSP; P06536; 1GDC.
DR InterPro; IPR001103; Andrgn_receptor.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF02166; Androgen_recep. 1.
DR Pfam; PF00104; hormone_rec. 1.
DR Pfam; PF00105; zfc4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid. 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT NON_TER 1
FT DOMAIN <1 347 MODULATING.
FT DNA_BIND 349 414 NUCLEAR RECEPTOR-TYPE.

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FT ZN\_PING 349 369 C4-TYPE.  
 FT ZN\_PING 365 409 C4-TYPE.  
 FT DOMAIN 480 709 LIGAND-BINDING.  
 FT DOMAIN 3 6 POLY-GLN.  
 FT DOMAIN 182 187 POLY-PRO.  
 FT DOMAIN 201 207 POLY-ALA.  
 FT DOMAIN 254 262 POLY-GLY.  
 SQ SEQUENCE 709 AA; 77391 MW; 4087666137E9786B CRC64;

Query Match 98.4%; Score 1349.5; DB 1; Length 709;  
 Best Local Similarity 99.6%; Pred. No. 2,4e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGYECOPIFLNTLEAIPGVVCAHDNNQPSFALLSINELGEROLVHVYKAK 61  
 DB 452 SH-IBGYECOPIFLNTLEAIPGVVCAHDNNQPSFALLSINELGEROLVHVYKAK 510  
 QY 62 ALPGFRLHVDQMAVIOYSWGLMVFAMGWSFTVNSRMLYFAPDLVFNERYMHKSRM 121  
 DB 511 ALPGFRLHVDQMAVIOYSWGLMVFAMGWSFTVNSRMLYFAPDLVFNERYMHKSRM 570  
 QY 122 YSCVVRHLSQBFGLQITPQEFLOKALLFSIIIPVDGLKXKQFDELPMNYIKELDR 181  
 DB 571 YSCVVRHLSQBFGLQITPQEFLOKALLFSIIIPVDGLKXKQFDELPMNYIKELDR 630  
 QY 182 IIAKRNKPTSCSRFFQTLKLDVOPILARELHOFTFDLLIKSHMVSVDPEPMABITIS 241  
 DB 631 IIAKRNKPTSCSRFFQTLKLDVOPILARELHOFTFDLLIKSHMVSVDPEPMABITIS 690  
 QY 242 VOVPKILSGKVKPIYFHTQ 260  
 DB 691 VOVPKILSGKVKPIYFHTQ 709

RESULT 2  
 ANDR\_EULFC STANDARD; PRT; 884 AA.  
 AC 09776;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Androgen receptor (Dihydrotestosterone receptor).  
 GN AR OR NR3C4.  
 OS Eulemur fulvus collaris (Collared brown lemur).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Eulemur.  
 NCBI\_TaxID=47178;  
 RX MEDLINE=98404153; PubMed=9732460;  
 RA Choong C.S., Kempainen J.A., Wilson E.M.;  
 RT "Evolution of the primate androgen receptor: a structural basis for  
 disease.";  
 RL J. Mol. Evol. 47:334-342(1998).  
 CC - FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
 CC - SUBCELLULAR LOCATION: Nuclear.  
 CC - DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC - SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 subfamily.  
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 CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
 CC EMBL; U94178; AAC73049.1; -  
 DR HSSP; P06536; IGDC.

DR TRANSFAC; T04655; -  
 DR InterPro; IPR001103; Andrgn\_receptor.  
 DR InterPro; IPR00536; Hormone\_rec\_1lg.  
 DR InterPro; IPR011723; Stdhnm\_receptor.  
 DR InterPro; IPR01628; ZnF\_Casteroid.  
 DR Pfam; PF02166; Androgen\_recep. 1.  
 DR Pfam; PF02164; hormone\_rec. 1.  
 DR Pfam; PF0105; zF-CA; 1.  
 DR PRINTS; PR00398; STRODHOMER.  
 DR PRINTS; PR00047; STROIDPINGER.  
 DR Prodom; PD000035; ZnF\_Casteroid; 1.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; ZnF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 FT ZINC-FINGER; Steroid-binding.  
 FT DOMAIN 1 522 MODULATING (BY SIMILARITY).  
 FT DNA\_BIND 524 589 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_PING 524 544 C4-TYPE.  
 FT ZN\_PING 560 584 C4-TYPE.  
 FT ZN\_PING 560 584 C4-TYPE.  
 FT DOMAIN 55 58 LIGAND-BINDING.  
 FT DOMAIN 55 58 POLY-GLN.  
 FT DOMAIN 64 70 POLY-GLN.  
 FT DOMAIN 116 120 POLY-ALA.  
 FT DOMAIN 174 178 POLY-GLN.  
 FT DOMAIN 353 362 POLY-PRO.  
 FT DOMAIN 379 383 POLY-ALA.  
 FT DOMAIN 408 411 POLY-ALA.  
 FT DOMAIN 430 435 POLY-GLY.  
 SQ SEQUENCE 884 AA; 95610 MW; 18F570E352FAD2BD CRC64;

Query Match 98.4%; Score 1349.5; DB 1; Length 884;  
 Best Local Similarity 99.6%; Pred. No. 3.1e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGYECOPIFLNTLEAIPGVVCAHDNNQPSFALLSINELGEROLVHVYKAK 61  
 DB 627 SH-IBGYECOPIFLNTLEAIPGVVCAHDNNQPSFALLSINELGEROLVHVYKAK 685  
 QY 62 ALPGFRLHVDQMAVIOYSWGLMVFAMGWSFTVNSRMLYFAPDLVFNERYMHKSRM 121  
 DB 686 ALPGFRLHVDQMAVIOYSWGLMVFAMGWSFTVNSRMLYFAPDLVFNERYMHKSRM 745  
 QY 122 YSCVVRHLSQBFGLQITPQEFLOKALLFSIIIPVDGLKXKQFDELPMNYIKELDR 181  
 DB 746 YSCVVRHLSQBFGLQITPQEFLOKALLFSIIIPVDGLKXKQFDELPMNYIKELDR 805  
 QY 182 IIAKRNKPTSCSRFFQTLKLDVOPILARELHOFTFDLLIKSHMVSVDPEPMABITIS 241  
 DB 806 IIAKRNKPTSCSRFFQTLKLDVOPILARELHOFTFDLLIKSHMVSVDPEPMABITIS 865  
 QY 242 VOVPKILSGKVKPIYFHTQ 260  
 DB 866 VOVPKILSGKVKPIYFHTQ 884

RESULT 3  
 ANDR\_MACPA STANDARD; PRT; 895 AA.  
 AC 097952;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Androgen receptor (Dihydrotestosterone receptor).  
 GN AR OR NR3C4.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 NCBI\_TaxID=9541;  
 RX MEDLINE=98404153; PubMed=9732460;  
 RP SEQUENCE FROM N.A.  
 DR HSSP; P06536; IGDC.

RA Choong C.S., Kempainen J.A., Wilson B.M.;  
 RT "Evolution of the primate androgen receptor: a structural basis for  
 RT disease.";  
 RL J. Mol. Evol. 47:334-342(1998).  
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 CC subfamily.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U94179; AAC73050.1; -  
 CC HSSP; P06536; IGDC.  
 CC TRANSFAC; T04654; -  
 CC InterPro; IPR001103; Andrgn\_receptor.  
 CC InterPro; IPR000536; Hormone\_rec\_119.  
 CC InterPro; IPR001628; Znf\_C4steroid.  
 CC Pfam; PF02166; Androgen\_Recep; 1.  
 CC Pfam; PF00104; hormone\_rec; 1.  
 CC Pfam; PF00105; Zf-C4; 1.  
 CC PRINTS; PR00047; STEROIDINGER.  
 CC PRODOM; PD000035; Znf\_C4steroid; 1.  
 CC SMART; SM00430; HOL1; 1.  
 CC SMART; SM00399; ZNF\_C4; 1.  
 CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 CC Zinc-finger; Steroid-binding.  
 CC MODULATING (BY SIMILARITY).  
 CC NUCLEAR RECEPTOR-TYPE.  
 CC C4-TYPE.  
 CC C4-TYPE.  
 CC C4-TYPE.  
 CC LIGAND-BINDING.  
 CC POLY-GLN.  
 CC POLY-GLN.  
 CC POLY-GLN.  
 CC POLY-PRO.  
 CC POLY-ALA.  
 CC POLY-GLY.  
 CC SEQUENCE 895 AA; 96494 MW; A3EB17916F43A097 CRC64;  
 SO  
 Query Match 98.4%; Score 1349.5; DB 1; Length 895;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SHMIEGYECOPILFVLAIEBEGVACAGHNDNPPSPALLSLNIELEGEROLVHVYKAK 61  
 DB 638 SH-IEGYECOPILFVLAIEBEGVACAGHNDNPPSPALLSLNIELEGEROLVHVYKAK 696  
 QY 62 ALPGFRNLAVDDQNAVIOYMWGLVWPAWGMSFTNVNSRMLYFAPDLVFNEMKSRM 121  
 DB 697 ALPGFRNLAVDDQNAVIOYMWGLVWPAWGMSFTNVNSRMLYFAPDLVFNEMKSRM 756  
 QY 122 YSQCVRMHLSOEERFMLOITPOEFLCMKALLFSIIPVDGKKNQFPDELKMYIKELDR 181  
 DB 757 YSQCVRMHLSOEERFMLOITPOEFLCMKALLFSIIPVDGKKNQFPDELKMYIKELDR 816  
 QY 182 IIAKCRKNPTSCSRFYQITKLDSVQPIARELHOFTEFLIKSHMVSVDPENMAATIS 241  
 DB 817 IIAKCRKNPTSCSRFYQITKLDSVQPIARELHOFTEFLIKSHMVSVDPENMAATIS 876  
 QY 242 VQVPKILSGKVPYIFHTQ 260  
 DB 877 VQVPKILSGKVPYIFHTQ 895

RESULT 4  
 ANDR\_PAPHA STANDARD; PRT; 895 AA.  
 AC 097960;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Androgen receptor (Dihydrotestosterone receptor).  
 GN AR OR NR3C4.  
 OS Papio hamadryas (Hamadryas baboon).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Papio.  
 NC NCBI\_TaxID=9557;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98404153; PubMed=9732460;  
 RA Choong C.S., Kempainen J.A., Wilson B.M.;  
 RT "Evolution of the primate androgen receptor: a structural basis for  
 RT disease.";  
 RL J. Mol. Evol. 47:334-342(1998).  
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 CC subfamily.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U94179; AAC73047.1; -  
 CC HSSP; P06536; IGDC.  
 CC TRANSFAC; T04652; -  
 CC InterPro; IPR001103; Andrgn\_receptor.  
 CC InterPro; IPR000536; Hormone\_rec\_119.  
 CC InterPro; IPR001628; Znf\_C4steroid.  
 CC Pfam; PF02166; Androgen\_Recep; 1.  
 CC Pfam; PF00104; hormone\_rec; 1.  
 CC Pfam; PF00105; Zf-C4; 1.  
 CC PRINTS; PR00047; STEROIDINGER.  
 CC PRODOM; PD000035; Znf\_C4steroid; 1.  
 CC SMART; SM00430; HOL1; 1.  
 CC SMART; SM00399; ZNF\_C4; 1.  
 CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 CC Zinc-finger; Steroid-binding.  
 CC MODULATING (BY SIMILARITY).  
 CC NUCLEAR RECEPTOR-TYPE.  
 CC C4-TYPE.  
 CC C4-TYPE.  
 CC C4-TYPE.  
 CC LIGAND-BINDING.  
 CC POLY-GLN.  
 CC POLY-GLN.  
 CC POLY-GLN.  
 CC POLY-PRO.  
 CC POLY-ALA.  
 CC POLY-GLY.  
 CC SEQUENCE 895 AA; 96478 MW; 9020C0DC6711B5D CRC64;  
 SO  
 Query Match 98.4%; Score 1349.5; DB 1; Length 895;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGECQPIFLNVLKALRPGVACAGHNDNPPDSFALLSSINELGEROLVHVVKAK 61  
 DB 638 SH-1EGYECQPIFLNVLKALRPGVACAGHNDNPPDSFALLSSINELGEROLVHVVKAK 696  
 QY 62 ALPGFRNLAVDDQNAVIOYSWGMGLVFMGWRSPFTVNSRMLYFAPDLVFNRYMHKSRM 121  
 DB 697 ALPGFRNLAVDDQNAVIOYSWGMGLVFMGWRSPFTVNSRMLYFAPDLVFNRYMHKSRM 756  
 QY 122 YSQCYRMHLSQBFGLQITPOEFLCKMALLPSIIPVDGLKXKQFDELMMNYIKELDR 181  
 DB 757 YSQCYRMHLSQBFGLQITPOEFLCKMALLPSIIPVDGLKXKQFDELMMNYIKELDR 816  
 QY 182 IIAKCRKNPSCSRPFQTLKLDVOPILAREHOFTEPLLKSHMVSVDPEMMAEITIS 241  
 DB 817 IIAKCRKNPSCSRPFQTLKLDVOPILAREHOFTEPLLKSHMVSVDPEMMAEITIS 876  
 QY 242 VQVPKILSGKVKPIYFHTQ 260  
 DB 877 VQVPKILSGKVKPIYFHTQ 895

RESULT 5  
 ID ANDR MOUSE STANDARD; PRT; 899 AA.  
 AC PI9051:  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Androgen receptor (Dihydrotestosterone receptor).  
 GN AR OR NR3C4.  
 OS Mus musculus (Mouse).  
 QC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c;  
 RA MEDLINE=90386642; PubMed=2403358;  
 RA He W.W., Fischer U.M., Sun S., Bihartz D.L., Zhu X., Young C.Y.F.,  
 RA Kelley D.B., Tindall D.J.;  
 RT "Molecular cloning of androgen receptors from divergent species with  
 RT a polymerase chain reaction technique: complete cDNA sequence of the  
 RT mouse androgen receptor and isolation of androgen receptor cDNA  
 RT probes from dog, guinea pig and clawed frog";  
 RL Biochem. Biophys. Res. Commun. 171:697-704(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=91133433; PubMed=2178222;  
 RA Gaspar M.L., Mo T., Toai M.;  
 RA "Structure and size distribution of the androgen receptor mRNA in  
 RT wild-type and Tfm/Y mutant mice";  
 RL Mol. Endocrinol. 4:1600-1610(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=91354214; PubMed=1883336;  
 RA Faber P.W., King A., van Rooij H.C.J., Brinkmann A.O., de Boer N.J.,  
 RA Trapman J.;  
 RT "The mouse androgen receptor. Functional analysis of the protein and  
 RT characterization of the gene";  
 RL Biochem. J. 278:269-278(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=92017874; PubMed=1681426;  
 RA Charest N.J., Zhou Z., Lubahn D.B., Olsen K.L., Wilson E.M.,  
 RA French F.S.;  
 RT "A frameshift mutation destabilizes androgen receptor messenger RNA  
 RT in the Tfm mouse";  
 RL Mol. Endocrinol. 5:573-581(1991).  
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,

CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -1- MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS  
 CC ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;  
 CC HORMONE-BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE  
 CC HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA  
 CC SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 CC subfamily.  
 CC -----  
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 CC send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL: S56585; AAB19916.1; -;  
 CC EMBL: X53779; CA37795.1; -;  
 CC EMBL: M37890; AAA37234.1; -;  
 CC EMBL: X59592; CA42160.1; -;  
 CC DR PIR: A35895; A35895.  
 CC HSSP: P06536; 1GDC.  
 CC TRANSFAC: T00041; -;  
 CC MGD: MGI:88064; Ar.  
 CC InterPro: IPR001103; Andrgn\_receptor.  
 CC InterPro: IPR000536; Hormone\_rec\_1lg.  
 CC InterPro: IPR01628; Znf\_C4steroid.  
 CC Pfam: PF02166; Androgen\_recep. 1.  
 CC Pfam: PF00104; hormone\_rec. 1.  
 CC Pfam: PF00105; zf-C4. 1.  
 CC PRINTS: PR00047; STEROIDFINGER.  
 CC PRODOM: PD000035; Znf\_C4steroid. 1.  
 CC SMART: SM00430; HOL1. 1.  
 CC SMART: SM00399; ZNF C4. 1.  
 CC PROSITE: PS00031; NUCLEAR RECEPTOR; 1.  
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 CC Zinc-finger; Steroid-binding.  
 CC MODULATING (BY SIMILARITY).  
 CC NUCLEAR RECEPTOR-TYPE.  
 CC C4-TYPE.  
 CC C4-TYPE.  
 CC C4-TYPE.  
 CC LIGAND-BINDING.  
 CC POLY-ARG.  
 CC POLY-GLN.  
 CC POLY-PRO.  
 CC POLY-ALA.  
 CC POLY-GLY.  
 CC SEQUENCE 899 AA; 98193 MW; FD9EE07C07F7A568 CRC64;  
 SQ  
 Query Match 98.4%; Score 1349.5; DB 1; Length 899;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SHMIEGECQPIFLNVLKALRPGVACAGHNDNPPDSFALLSSINELGEROLVHVVKAK 61  
 DB 642 SH-1EGYECQPIFLNVLKALRPGVACAGHNDNPPDSFALLSSINELGEROLVHVVKAK 700  
 QY 62 ALPGFRNLAVDDQNAVIOYSWGMGLVFMGWRSPFTVNSRMLYFAPDLVFNRYMHKSRM 121  
 DB 701 ALPGFRNLAVDDQNAVIOYSWGMGLVFMGWRSPFTVNSRMLYFAPDLVFNRYMHKSRM 760  
 QY 122 YSQCYRMHLSQBFGLQITPOEFLCKMALLPSIIPVDGLKXKQFDELMMNYIKELDR 181  
 DB 761 YSQCYRMHLSQBFGLQITPOEFLCKMALLPSIIPVDGLKXKQFDELMMNYIKELDR 820  
 QY 182 IIAKCRKNPSCSRPFQTLKLDVOPILAREHOFTEPLLKSHMVSVDPEMMAEITIS 241  
 DB 821 IIAKCRKNPSCSRPFQTLKLDVOPILAREHOFTEPLLKSHMVSVDPEMMAEITIS 880  
 QY 242 VQVPKILSGKVKPIYFHTQ 260  
 DB 881 VQVPKILSGKVKPIYFHTQ 899

RESULT 6  
 ANDR\_RAT STANDARD; PRT; 902 AA.  
 AC P15257; 063049; 14, Created)  
 DT 01-APR-1990 (Rel. 14, last sequence update)  
 DT 01-APR-1990 (Rel. 14, last sequence update)  
 DT 15-SEP-2003 (Rel. 42, last annotation update)  
 DE Androgen receptor (Dihydrotestosterone receptor).  
 GN AR OR NR3C4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxId=10116;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=69112209; PubMed=3216867;  
 RA Tan J., Joseph D.R., Quarmby V.E., Lubahn D.B., Sar M., French F.S.,  
 RA Wilson E.M.;  
 RA "The rat androgen receptor: primary structure, autoregulation of its  
 RT messenger ribonucleic acid, and immunocytochemical localization of  
 RT the receptor protein.";  
 RL Mol. Endocrinol. 2:1276-1285 (1988).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=89017168; PubMed=3174628;  
 RX Chang C., Kokontis J., Iiao S.;  
 RT "Structural analysis of complementary DNA and amino acid sequences of  
 RT human and rat androgen receptors.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215 (1988).  
 [3]  
 RP SEQUENCE FROM N.A.; AND VARIANT TFM GLN-735.  
 RX MEDLINE=90256822; PubMed=2341409;  
 RX Lubahn D.B., Olsen K.L., French F.S., Wilson E.M.;  
 RA "A single base mutation in the androgen receptor gene causes androgen  
 RT insensitivity in the testicular feminized rat.";  
 RL J. Biol. Chem. 265:8893-8900 (1990).  
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN THE SEMINAL VESICLE,  
 CC VENTRAL PROSTATE AND COAGULATING GLAND WITH LOWER LEVELS IN THE  
 CC KIDNEY, AND LEVATOR ANI MUSCLE.  
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -1- DISEASE: Defects in AR are a cause of androgen insensitivity. Rats  
 CC with this syndrome are called testicular feminized (TFM).  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 CC subfamily.  
 CC -----  
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 CC -----  
 CC EMBL, M20133; AAA40733.1; -  
 CC EMBL, M23264; AAA40759.1; -  
 CC EMBL, J05454; AAA40734.1; -  
 CC PIR, B40494; B40494.  
 CC PDB, 1137; 02-MAY-01.  
 CC PDB, 1138; 02-MAY-01.  
 CC TRANSFAC; T00042; -  
 CC InterPro; IPR001103; Andrgn\_receptor.  
 CC InterPro; IPR000536; Hormone\_rec\_119.  
 CC InterPro; IPR001628; Znf\_CsteroiId.  
 CC Pfam; PF02166; Androgen\_recep; 1.

DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00047; STROIDPINGER.  
 DR Prodom; PD000035; Znf\_CsteroiId; 1.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; Znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Steroid-binding; Disease mutation; 3D-structure.  
 FT DOMAIN 1 540  
 FT DNA\_BIND 542 607 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 542 562 C4-TYPE.  
 FT ZN\_FING 578 602 C4-TYPE.  
 FT DOMAIN 673 902 LIGAND-BINDING.  
 FT DOMAIN 63 67 POLY-ARG.  
 FT DOMAIN 174 195 POLY-GLN.  
 FT DOMAIN 370 376 POLY-PRO.  
 FT DOMAIN 394 400 POLY-ALA.  
 FT DOMAIN 444 450 POLY-GLY.  
 FT VARIANT 735 735 R -> Q (IN TFM, HAS ONLY 10-15% OF THE  
 FT ANDROGEN-BINDING CAPACITY OF WILD-TYPE  
 FT AR).  
 FT CONFLICT 195 195 MISSING (IN REF. 3).  
 FT CONFLICT 389 389 S -> L (IN REF. 2).  
 SQ SEQUENCE 902 AA; 98217 MW; 43F4064759FDCBD CRC64;  
 Query Match 98.4%; Score 1349.5; DB 1; Length 902;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SHMIGYECOPFLANVLAIEPGVVCAGHDNNDPSFALSSINLEGEROLVHYVYKAK 61  
 DB 645 SH-IRGYECOPFLANVLAIEPGVVCAGHDNNDPSFALSSINLEGEROLVHYVYKAK 703  
 QY 62 ALPGFRNLVDDQNAVIOYSWGLVFMGWRSPFTNVNSRMUYAPDLVFNERYMKSRM 121  
 DB 704 ALPGFRNLVDDQNAVIOYSWGLVFMGWRSPFTNVNSRMUYAPDLVFNERYMKSRM 763  
 QY 122 YSQCRMHLSQSRGWLQITPOEFLCMKALLFSTIPDGLKNGKFPBELMNYIKELDR 181  
 DB 764 YSQCRMHLSQSRGWLQITPOEFLCMKALLFSTIPDGLKNGKFPBELMNYIKELDR 823  
 QY 182 IIAKCRKPTSCSRFPYLTGLDSVQPIARELHQFFDLIKSHMVSVDPEMMAIITS 241  
 DB 824 IIAKCRKPTSCSRFPYLTGLDSVQPIARELHQFFDLIKSHMVSVDPEMMAIITS 883  
 QY 242 VQVPKILSGKVPYIFHTQ 260  
 DB 884 VQVPKILSGKVPYIFHTQ 902  
 RESULT 7  
 ANDR\_CANFA STANDARD; PRT; 907 AA.  
 AC 09T750;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, last sequence update)  
 DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Androgen receptor (Dihydrotestosterone receptor).  
 GN AR OR NR3C4.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxId=9615;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21618348; PubMed=11768233;  
 RA Lu B., Smock S.L., Castleden T.A., Owen T.A.;  
 RT "Molecular cloning and functional characterization of the canine  
 RT androgen receptor.";  
 RL Mol. Cell. Biochem. 226:129-140 (2001).  
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR

	CC	PROBABLE LOCATION: Nuclear.
	CC	-1- SUBCELLULAR LOCATION: Nuclear.
	CC	-1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
	CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
	CC	-1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
	CC	subfamily.
	CC	-----
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	CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .
	CC	-----
	DR	EMBL; AF197950; AAFL8084.1; --
	DR	HSSP; P06536; IGDC.
	DR	InterPro; IPR001103; Andrgn_receptor.
	DR	InterPro; IPR000536; Hormone_rec_1lg.
	DR	InterPro; IPR001628; Znf_Casteroid.
	DR	Pfam; PF02116; Androgen_recep. 1.
	DR	Pfam; PF00104; hormone_rec. 1.
	DR	Pfam; PF00105; zf-C4; 1.
	DR	PRINTS; PR00047; STEROIDINGER.
	DR	ProDom; PD000035; Znf_Casteroid; 1.
	DR	SMART; SMO0430; HOL1; 1.
	DR	SMART; SMO0399; Znf_C4; 1.
	DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
	KW	Receptor; Transcription regulation; DNA-binding; Nuclear protein;
	KM	Zinc-finger; Steroid-binding.
	FT	DOMAIN 1 545 MODULATING (BY SIMILARITY).
	FT	DNA_BIND 547 612 NUCLEAR RECEPTOR-TYPE.
	FT	ZN_FING 547 567 C4-TYPE.
	FT	ZN_FING 583 607 C4-TYPE.
	FT	DOMAIN 678 907 LIGAND-BINDING.
	FT	DOMAIN 55 76 POLY-GLN.
	FT	DOMAIN 70 76 POLY-GLN.
	FT	DOMAIN 131 134 POLY-GLN.
	FT	DOMAIN 180 202 POLY-GLN.
	FT	DOMAIN 329 332 POLY-SER.
	FT	DOMAIN 375 384 POLY-PRO.
	FT	DOMAIN 399 405 POLY-ALA.
	SQ	SEQUENCE 907 AA; 98726 MW; C6619F78DD2338AF CRC64;
		Query Match 98.4%; Score 1349.5; DB 1; Length 907;
		Best Local Similarity 99.6%; Pred. No. 3.2e-118;
		Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1
Oy	2	SHMIIEGYSCTPIFNVLVAIRBGVCAAGHDNNQPDSFALLSLINELGEROLVHYVKAK 61
Db	650	SH-IRGYICQPIFNVLVAIRBGVCAAGHDNNQPSFALLSSLINELGEROLVHYVKAK 708
Oy	62	ALPGFRNLHVDDQMAVIQYSNWGLVFPAMGWRSPTNVNSRMLYEAPDLVFNEYRHKSRM 121
Db	709	ALPGFRNLHVDDQMAVIQYSNWGLVFPAMGWRSPTNVNSRMLYEAPDLVFNEYRHKSRM 768
Oy	122	YSQCRRMHLSQSEFGMLQTPQEPFCMKATLLFSIIIPVGLKNQKPPPELRMMYIKELDR 181
Db	769	YSQCRRMHLSQSEFGMLQTPQEPFCMKATLLFSIIIPVGLKNQKPFDELRMMYIKELDR 828
Oy	182	IACKRKNPSCSRREPYQLTKLDSVOPIARELHQFTPLLTKSHNVSVDPEEMAETIS 241
Db	829	IACKRKNPSCSRREPYQLTKLDSVOPIARELHQFTPLLTKSHNVSVDPEEMAETIS 888
Oy	242	VQVPKLISGRKVPRIYFHQ 260
Db	889	VQVPKLISGRKVPRIYFHQ 907
		RESULT 8
ID	ANDR_PANTR	
ID	ANDR_PANTR	
AC	097775;	
	STANDARD;	FRT; 911 AA.

DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Androgen receptor (Dihydrotestosterone receptor).  
GN AR OR NR3C4.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
OX NCBI\_TaxID:9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98404153; PubMed=9732460;  
RA Choong C.S., Kempainen J.A., Wilson B.M.;  
RT "Evolution of the primate androgen receptor: a structural basis for  
RT disease.";  
RL J. Mol. Evol. 47:334-342(1998).  
CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
CC subfamily.  
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CC -----  
DR EMBL; U94177; AAC73048.1; -.  
DR HSSP; P06536; IGDC.  
DR TRANSFAC; T04653; -.  
DR InterPro; IPR001103; Andrgn\_receptor.  
DR InterPro; IPR000536; Hormone\_rec\_1sf.  
DR InterPro; IPR001628; Znf\_C4steroid.  
DR Pfam; PF02166; Androgen\_rec; 1.  
DR Pfam; PF00104; hormone\_rec; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00047; STROIDFRINGER.  
DR ProDom; PD000035; Znf\_C4steroid; 1.  
DR SMART; SM00430; HOL1; 1.  
DR SMART; SM00399; Znf\_C4; 1.  
DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
KW Zinc-finger; Steroid-binding.  
KW DOMAIN 1 549 MODULATING (BY SIMILARITY).  
FT FT DNA BIND 551 616 NUCLEAR RECEPTOR-TYPE.  
FT FT ZN\_FING 551 571 C4-TYPE.  
FT FT ZN\_FING 587 611 C4-TYPE.  
FT FT DOMAIN 682 911 LIGAND-BINDING.  
FT FT DOMAIN 57 78 POLY-GLN.  
FT FT DOMAIN 84 88 POLY-GLN.  
FT FT DOMAIN 192 196 POLY-GLN.  
FT FT DOMAIN 371 380 POLY-PRO.  
FT FT DOMAIN 395 401 POLY-ALA.  
FT FT DOMAIN 448 464 POLY-GLY.  
SO SEQUENCE 911 AA; 98402 MW; 601BBDABE697DAA4 CRC64;  
Query Match 98.4%; Score 1349.5; DB 1; Length 911;  
Best Local Similarity 99.6%; Pred. No. 3.2e-118;  
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 2 SHMIEGTCOPIPFANTKATIEPGVCGGHNNODSPALLISLNELGEROLVHVVKAK 61  
DB 654 SH-IEGYECOPIFLVNLEAIEPGVCGGHNNODSPALLISLNELGEROLVHVVKAK 712  
QY 62 ALPEFRKLAVDDQAAVLYQYSWGLMVAVMGKRSFTTNNSRLYAPDLVFEFYMHSKSM 121  
DB 713 ALPEFRKLAVDDQAAVLYQYSWGLMVAVMGKRSFTTNNSRLYAPDLVFEFYMHSKSM 772



QY 122 YSCVAMRHLSORFGWLOITPQFLCKAKALLFPIIPVDGLKQKQFDELMNYIKELDR 181  
 DB 773 YSCVAMRHLSORFGWLOITPQFLCKAKALLFPIIPVDGLKQKQFDELMNYIKELDR 832  
 QY 182 IIAKCKRNPTGCGRRRYOLTKLDSVQPIARELHQTFFDLILKSHVSVDFPMMAEITS 241  
 DB 833 IIAKCKRNPTGCGRRRYOLTKLDSVQPIARELHQTFFDLILKSHVSVDFPMMAEITS 892  
 QY 242 VQVPKILSGVKRPIYFHTQ 260  
 DB 893 VQVPKILSGVKRPIYFHTQ 911  
 RESULT 9  
 ANDR\_HUMAN STANDARD; PRT; 919 AA.  
 ID P10275;  
 AC 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Androgen receptor (Dihydrotestosterone receptor).  
 GN AR OR NR3C4 OR DHTR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89112208; PubMed=3216866;  
 RA Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E.,  
 RA French P.S., Wilson E.M.;  
 RT "The human androgen receptor: complementary deoxyribonucleic acid  
 RT cloning, sequence analysis and gene expression in prostate.";  
 RT Mol. Endocrinol. 2:1265-1275(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT CAIS MET-866.  
 RX MEDLINE=90083302; PubMed=2594783;  
 RA Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J.,  
 RA Wilson E.M., French P.S.;  
 RT "Sequence of the intron/exon junctions of the coding region of the  
 RT human androgen receptor gene and identification of a point mutation  
 RT in a family with complete androgen insensitivity.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90258935; PubMed=2342476;  
 RA Govindan M.V.;  
 RT "Specific region in hormone binding domain is essential for hormone  
 RT binding and trans-activation by human androgen receptor.";  
 RT Mol. Endocrinol. 4:417-427(1990).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=prostate;  
 MEDLINE=89017168; PubMed=3174628;  
 RA Chang C., Kokontis J., Liao S.;  
 RT "Structural analysis of complementary DNA and amino acid sequences of  
 RT human and rat androgen receptors.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=prostate;  
 MEDLINE=89098909; PubMed=2911578;  
 RA Tilley W.D., Marcelli M., Wilson J.D., McPhaul M.J.;  
 RT "Characterization and expression of a cDNA encoding the human androgen  
 RT receptor.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 86:327-331(1989).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=prostate;  
 MEDLINE=91155943; PubMed=2293020;  
 RA Marcelli M., Tilley W.D., Wilson C.M., Griffin J.E., Wilson J.D.,  
 RA McPhaul M.J.;

RT "Definition of the human androgen receptor gene structure permits the  
 RT identification of mutations that cause androgen resistance: premature  
 RT termination of the receptor protein at amino acid residue 588 causes  
 RT complete androgen resistance.";  
 RT Mol. Endocrinol. 4:1105-1116(1990).  
 RN [7]  
 RP SEQUENCE OF 189-919 FROM N.A.  
 RX MEDLINE=8817811; PubMed=3353726;  
 RA Chang C., Kokontis J., Liao S.;  
 RT "Molecular cloning of human and rat complementary DNA encoding  
 RT androgen receptors.";  
 RT Science 240:324-326(1988).  
 RN [8]  
 RP SEQUENCE OF 468-919 FROM N.A.  
 RX MEDLINE=88240407; PubMed=3377788;  
 RA Trapman J., Klaassen P., Kuiper G.G.J.M., van der Kout J.A.G.M.,  
 RA Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voohtorst M.M.,  
 RA Mulder E., Brinkmann A.O.;  
 RT "Cloning, structure and expression of a cDNA encoding the human  
 RT androgen receptor.";  
 RT Biochem. Biophys. Res. Commun. 153:241-248(1988).  
 RN [9]  
 RP INTERACTION WITH RAN.  
 RX MEDLINE=99329028; PubMed=10400640;  
 RA Hsiao P.-W., Lin D.-L., Nakao R., Chang C.;  
 RT "The linkage of Kennedy's neuron disease to ARA24, the first  
 RT identified androgen receptor polyglutamine region-associated  
 RT coactivator.";  
 RT J. Biol. Chem. 274:20229-20234(1999).  
 RN [10]  
 RP POLYMORPHISM OF POLY-GLN REGION.  
 RX MEDLINE=92220629; PubMed=1561105;  
 RA Slidders H.F.B.M., Oosterla B.A., Brinkmann A.O., Trapman J.;  
 RT "Trinucleotide repeat polymorphism in the androgen receptor gene  
 RT (AR)."  
 RT Nucleic Acids Res. 20:1427-1427(1992).  
 RN [11]  
 RP POLYMORPHISM OF POLY-GLY REGION.  
 RX TISSUE=Blood.  
 RA Lu J., Daniels M.;  
 RT "Submitted (Feb-1995) to the EMBL/GenBank/DBJ databases."  
 RN [12]  
 RP POLYMORPHISM OF POLY-GLN REGION.  
 RX MEDLINE=97250535; PubMed=9096391;  
 RA Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Brufsky A.,  
 RA Talcott J., Hennekens C.H., Kantoff P.W.;  
 RT "The CAG repeat within the androgen receptor gene and its  
 RT relationship to prostate cancer.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 94:3320-3323(1997).  
 RN [13]  
 RP ERRATUM.  
 RA Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Dahl D.,  
 RA Brufsky A., Talcott J., Hennekens C.H., Kantoff P.W.;  
 RT Proc. Natl. Acad. Sci. U.S.A. 94:8272-8272(1997).  
 RN [14]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=93092459; PubMed=1458719;  
 RA Pinsky L., Trifiro M.A., Kautman M., Beltel L.K., Matre A.,  
 RA Kazemi-Bafarjani P., Sabaghian N., Lombroso R., Alvarado C.,  
 RA Vasiliou M., Gottlieb B.;  
 RT "Androgen resistance due to mutation of the androgen receptor.";  
 RT Clin. Invest. Med. 15:456-472(1992).  
 RN [15]  
 RP REVIEW ON VARIANTS AIS.  
 RX MEDLINE=93333360; PubMed=8339746;  
 RA Brown T.R., Scherer P.A., Chang Y.-T., Migeon C.J., Ghirri P.,  
 RA Muroto K., Zhou Z.;  
 RT "Molecular genetics of human androgen insensitivity.";  
 RT Eur. J. Pediatr. 152 Suppl. 2:S62-S69(1993).  
 RN [16]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=94059770; PubMed=8240973;  
 RA Sultan C., Lombroso S., Poujol N., Belon C., Boudon C.,



RA Lobaccaro J.-M.;  
 RT "Mutations of androgen receptor gene in androgen insensitivity  
 syndromes";  
 RL J. Steroid Biochem. Mol. Biol. 46:519-530(1993).  
 RN [17]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=95023089; PubMed=7937057;  
 RA Patterson M.N., Hughes I.A., Gotlib B., Pinsky L.;  
 RT "The androgen receptor gene mutations database";  
 RL Nucleic Acids Res. 22:3560-3562(1994).  
 RN [18]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=95352489; PubMed=7626493;  
 RA Brinkmann A.O., Jenster G., Ris-Stalpers C., van der Korput J.A.G.M.,  
 RT Bruggenwirth H.T., Boemer A.L.M., Trapman J.;  
 RL "Androgen receptor mutations";  
 RN J. Steroid Biochem. Mol. Biol. 53:443-446(1995).  
 RP [19]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=97169385; PubMed=9016528;  
 RA Gotlib B., Trifiro M.A., Lombroso R., Vasiljov D.M., Pinsky L.;  
 RT "The androgen receptor gene mutations database";  
 RL Nucleic Acids Res. 25:158-162(1997).  
 RN [20]  
 RP VARIANT LNCAP ALA-877.  
 RX MEDLINE=91083633; PubMed=2260966;  
 RA Veldscholte J., Ris-Stalpers C., Kuiper G.G.J.M., Jenster G.,  
 RT Berrevoets C.A., Claassen E., van Rooij H.C.J., Trapman J.,  
 RA Brinkmann A.O., Mulder E.;  
 RT "A mutation in the ligand binding domain of the androgen receptor  
 human LNCAP cells affects steroid binding characteristics and  
 response to anti-androgens";  
 RL Biochem. Biophys. Res. Commun. 173:534-540(1990).  
 RN [21]  
 RP VARIANTS CAIS CVS-774; GUN-831 AND MET-866.  
 RX MEDLINE=91186983; PubMed=2082179;  
 RA Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J.,  
 RT Corten J.L.;  
 RT "Functional characterization of naturally occurring mutant androgen  
 receptors from subjects with complete androgen insensitivity";  
 RL Mol. Endocrinol. 4:1759-1772(1990).  
 RN [22]  
 RP VARIANT CVS-774.  
 RX MEDLINE=91310758; PubMed=1856263;  
 RA Marcelli M., Tilley W.D., Zoppi S., Griffin J.E., Wilson J.D.,  
 RT McPhaul M.J.;  
 RT "Androgen resistance associated with a mutation of the androgen  
 receptor at amino acid 772 (Arg-->Cys) results from a combination of  
 decreased messenger ribonucleic acid levels and impairment of  
 receptor function";  
 RL J. Clin. Endocrinol. Metab. 73:318-325(1991).  
 RN [23]  
 RP VARIANT CAIS PRO-617.  
 RX MEDLINE=91154385; PubMed=1999491;  
 RA Marcelli M., Zoppi S., Grino P.B., Griffin J.E., Wilson J.D.,  
 RT McPhaul M.J.;  
 RT "A mutation in the DNA-binding domain of the androgen receptor gene  
 causes complete testicular feminization in a patient with  
 receptor-positive androgen resistance";  
 RL J. Clin. Invest. 87:1123-1126(1991).  
 RN [24]  
 RP VARIANT PAIS CVS-763.  
 RX MEDLINE=91185626; PubMed=2010552;  
 RA McPhaul M.J., Marcelli M., Tilley W.D., Griffin J.E.,  
 RT Isidro-Gutierrez R.F., Wilson J.D.;  
 RT "Molecular basis of androgen resistance in a family with a qualitative  
 abnormality of the androgen receptor and responsive to high-dose  
 androgen therapy";  
 RL J. Clin. Invest. 87:1413-1421(1991).  
 RN [25]

Query Match 98.4%; Score 1349.5; DB 1; Length 919;  
 Best Local Similarity 99.6%; Pred. No. 3,3e-118;

Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SEMTEGTCOPFIPLANTBAIEPGV/CAGHNNQDPSAALLSSNTEGEGQLVHVYVYAK 61  
 DB 662 SH-IEGYECQPIPLANTBAIEPGV/CAGHNNQDPSAALLSSNTEGEGQLVHVYVYAK 720  
 QY 62 ALPGFRLVDDQNAVQYSGMGLMFMGWRSPFNNSRLYAPLPVFNEMYSRM 121  
 DB 721 ALPGFRLVDDQNAVQYSGMGLMFMGWRSPFNNSRLYAPLPVFNEMYSRM 780  
 QY 122 YSQCVNRHLQSQRGWLQTPQEF/CMKALLPSIIPVDGLKQKFPDELRMYIKELDR 181  
 DB 781 YSQCVNRHLQSQRGWLQTPQEF/CMKALLPSIIPVDGLKQKFPDELRMYIKELDR 840  
 QY 182 IIAKRRKPTSCSRFPQTLTLDVQPIAREHQFPDLIKSHNVSVDPEMAGIIS 241  
 DB 841 IIAKRRKPTSCSRFPQTLTLDVQPIAREHQFPDLIKSHNVSVDPEMAGIIS 900  
 QY 242 VQPKTISGKVKPYPFHQ 260  
 DB 901 VQPKTISGKVKPYPFHQ 919  
 RESULT 10  
 PRGR\_RABIT STANDARD; PRT; 930 AA.  
 AC P06186;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Progesterone receptor (PR).  
 GN PGR OR NR33.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CX NCBI\_Txid=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87067449; PubMed=3538016;  
 RA Loosfelt H., Atger M., Mierant M., Gulochon-Mantel A., Meriel C.,  
 RT Loget F., Benarous R., Milgrom E.;  
 RT "Cloning and sequence analysis of rabbit progesterone-receptor  
 complementary DNA";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9045-9049(1986).  
 CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
 PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 subfamily.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DB EMBL; M14547; AAA31443.1; -.  
 DB PIR; A25923; A25923.  
 DB HSSP; P06401; 1A28.  
 DB TRNSPAC; T00697; -.  
 DB InterPro; IPR000536; Hormone\_rec\_1lg.  
 DB InterPro; IPR000128; Progesterone\_receptor.  
 DB InterPro; IPR001723; Steroid\_receptor.  
 DB InterPro; IPR001628; Znf\_C4steroid.  
 DB Pfam; PF00104; hormone\_rec\_1.  
 DB Pfam; PF02161; Prog\_receptor\_1.  
 DB Pfam; PF00105; zf-C4\_1.  
 DB PRINTS; PR00396; STERHORMONER.

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DR PRINTS; PR00047; STEROIDRECEPTOR.
DR Prodom; PD000035; ZnF C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; ZnF C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
FT Zinc-finger; Steroid-binding.
FT DOMAIN 1 565 MODULATING, PRO-RICH.
FT DNA BIND 568 633 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 568 588 C4-TYPE.
FT ZN_FING 604 628 C4-TYPE.
FT DOMAIN 678 930 STEROID-BINDING.
FT DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 930 AA; 98666 MW; 644FP4C13BF2F883 CRC64;

Query Match 55.9%; Score 766; DB 1; Length 930;
Best Local Similarity 55.5%; Pred. No. 1.2e-63;
Matches 137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;

QY 12 PFIPLVLEALPEPVCAHNNQDPSPALLSSINELGHEQLVHVVMKALPGFRLAHV 71
DB 682 PFIPLVLEALPEPVCAHNNQDPSPALLSSINELGHEQLVHVVMKALPGFRLAHV 71
QY 72 DDGMANVQISWGLMVFPMGMSFTVNSMFLYAPDVLNENYRMKSRMYSQCVNRHL 131
DB 742 DDGITLIQSWMSLMVFGLMRSYKHSQGLYAPDVLNENYRMKSRMYSQCVNRHL 131
QY 133 SGRFGLQITRPFELCKALLPSIIPVDGLKQKPFDELKMYIKELDIACKRNPT 191
DB 802 POFVFLQVQSEBFLCKKVLILNTIPLBGLRSQSPFEEBRSYIELIYALIGRKGJV 861
QY 192 SCRRFQYQLTKLSDVOPARELHOFPLDLIKSHMVSVDPPMMAIISVQVXILSKG 251
DB 862 SSGRFYQLTKLSDVOPARELHOFPLDLIKSHMVSVDPPMMAIISVQVXILSKG 251
QY 252 VKPITVF 258
DB 922 VKPILTF 928

RESULT 11
PRGR HUMAN STANDARD; PRT; 933 AA.
ID PRGR_HUMAN STANDARD; PRT; 933 AA.
AC P06401; Q9UPF7; 01-JAN-1988 (Rel. 06, Created)
DR 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Progesterone receptor (PR).
DS Progesterone receptor (PR).
GN PGR OR NR3C3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=90228361; PubMed=2328727;
RA Kastner P., Kust A., Turcotte B., Stropp U., Tora L., Gronemeyer H.,
RA Chabon P.,
RT "Two distinct estrogen-regulated promoters generate transcripts
RT encoding the two functionally different human progesterone receptor
RT forms A and B.";
RL EMO J. 9:1603-1614(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87184565; PubMed=3551956;
RA Mirzahi M., Atger M., D'Aurion L., Loosfelt H., Meriel C.,
RA Firlanaky F., Guichon-Mantel A., Galibert F., Milgrom R.,
RT "Complete amino acid sequence of the human progesterone receptor
RT deduced from cloned cDNA.";
RL Biochem. Biophys. Res. Commun. 143:740-748(1987).
RN [3]
RP SEQUENCE FROM N.A.
RL Kieback D.G., Agoulnik I.U., Tong X.-W.;

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RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 682-933.
RX MEDLINE=98282128; PubMed=9620806;
RA Williams S.P., Sigler P.B.;
RT "Atomic structure of progesterone complexed with its receptor.";
RL Nature 393:392-396(1998).
CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=P06401-1; Sequence=Displayed;
CC Name=A;
CC IsoId=P06401-2; Sequence=VSP 003706;
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC -----
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CC -----
DR EMBL; X51730; CAA36018.1; -.
DR EMBL; M15716; AAA60081.1; -.
DR EMBL; AF015381; AAD01587.1; -.
DR PIR; S09971; QRHUP.
DR PDB; 1A28; 15-JUL-98.
DR PDB; 1B3K; 14-JUN-01.
DR TRANSFAC; T00696; -.
DR Genew; HGNC:8910; PGR.
DR MIM; 607311; -.
DR GO; GO:0003707; F:steroid hormone receptor activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000536; Hormone_rec_1lg.
DR InterPro; IPR00128; Progesterone_receptor.
DR InterPro; IPR001723; Steroid_receptor.
DR InterPro; IPR001628; ZnF C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF02161; Prog_receptor; 1.
DR Pfam; PF00105; ZF-C4; 1.
DR PRINTS; PR00398; STRDOMONER.
DR PRINTS; PR0047; STEROIDRECEPTOR.
DR Prodom; PD000035; ZnF C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; ZnF C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding; Phosphorylation; Alternative splicing;
KW 3D-structure; Polymorphism.
FT DOMAIN 1 566 MODULATING, PRO-RICH.
FT DNA BIND 567 632 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 567 587 C4-TYPE.
FT ZN_FING 603 627 C4-TYPE.
FT DOMAIN 681 933 STEROID-BINDING.
FT DOMAIN 183 187 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 41 41 PHOSPHORYLATION (BY CK).
FT MOD_RES 227 227 PHOSPHORYLATION (BY CK).
FT MOD_RES 232 232 PHOSPHORYLATION (BY CK).
FT MOD_RES 552 552 PHOSPHORYLATION (BY CK).
FT MOD_RES 793 793 PHOSPHORYLATION (BY CK).
FT VARSPLIC 1 164 Missing (in isoform A).
FT VARSPLIC 625 625 /FTid=VSP 003706.
R -> I (in dbSNP:2020874).

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QY 252 VKPIYFH 258  
DB 915 VKPLLFH 921

RESULT 13  
PRGR MOUSE STANDARD; PRT; 923 AA.

AC 000175;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-UTL-1999 (Rel. 38, Last annotation update)  
DE Progesterone receptor (PR).  
GN PGR OR NR3C3 OR PR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91299759; PubMed=2069958;  
RA Schoet D.R., Shivamala G., Schneider W., Parry G.;  
RT "Molecular cloning, sequence analyses, and expression of  
complementary DNA encoding murine progesterone receptor.";  
RL Biochemistry 30:7014-7020(1991).  
RN (2)  
RP SEQUENCE OF 1-9 FROM N.A.  
RC STRAIN=129/Sv;  
RX MEDLINE=95100931; PubMed=7802637;  
RA Hagihara K., Wu-Peng X.S., Funabashi T., Kato J., Pfaff D.W.;  
RT "Nucleic acid sequence and DNase hypersensitive sites of the 5'  
region of the mouse progesterone receptor gene.";  
RL Biochem. Biophys. Res. Commun. 205:1093-1101(1994).  
CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR  
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
subfamily.

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DR EMBL, M68915; AAA3971.1; -;  
DR EMBL, U12644; AAA66067.1; -;  
DR PIR, A39596; A39596.  
DR HSRF, F06401; 1A28.  
DR TRANSFAC; T04680; -;  
DR MGD; MGI:97567; Pgr.  
DR InterPro; IPR000536; Hormone\_rec.1lg.  
DR InterPro; IPR000128; Progesterone\_receptor.  
DR InterPro; IPR001723; Steroid\_receptor.  
DR InterPro; IPR001628; Znf\_C4steroid.  
DR Pfam; PF00104; hormone\_rec.1.  
DR Pfam; PF02161; Prog\_receptor.1.  
DR Pfam; PF00105; zf-C4.1.  
DR PRINTS; PR00398; STRDHOMONER.  
DR PRINTS; PR00047; STROIDPTNGER.  
DR ProDom; PD000035; Znf\_C4steroid.1.  
DR SMART; SM00430; HOL1.1.  
DR SMART; SM00399; ZNF\_C4.1.  
DR PROSITE; PS00031; NUCLEAR\_RECEPTOR.1.  
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
KW Zinc-finger; Steroid-binding.  
FT DOMAIN 1 556 MODULATING, PRO-RICH.

FT DNA BIND 557 622 NUCLEAR RECEPTOR-TYPE.  
FT ZN\_FING 557 577 CA-TYPE.  
FT ZN\_FING 557 593 CA-TYPE.  
FT DOMAIN 671 923 STEROID-BINDING.  
FT DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
SQ SEQUENCE 923 AA; 99073 MW; 9415F1ED343BEE3F CRC64;

Query Match 55.3%; Score 758; DB 1; Length 923;  
Best Local Similarity 55.1%; Pred. No. 6, 8e-63;  
Matches 136; Conservative 56; Mismatches 55; Indels 0; Gaps 0;

QY 12 PIFLNVLAIEPVGVCAGHNNQPSFALLSLNELSGROLVHVYKMAKALPGFNHLY 71  
DB 675 PFLINLMISRPDVIYAGHNDTKPDTSSSLSLNSINGRQLSLSVKMSKSLPGFNHLY 734  
QY 72 DPGMAVIOYSGNGLVFWPANGKTSFTNNVSRMLYFAPDLVFNRYKHSKMSYQCVRRHL 131  
DB 735 DDQITLIOYSWMSLVFGLGMSYKRVSGQMLYFAPDLILNQRKMLSPFSLCLTMQOI 794  
QY 132 SQEFGMLQITPQEFPLCMKALLFSLIPVYGLKNQKFPDELRMNYIKELDRITACRKNPT 191  
DB 795 PGEFVKLVTHREFLCMKVLMLNTTFLBGLSSQSFESMRSSYLRELKALGLRQGVV 854  
QY 192 SCSSRPYQVTKLDSVOPARLHQTEDLLIKSHWVSVDPEMMAIISVQPKILSGK 251  
DB 855 PPSGRFYQVTKLDSLHDLVQGLHYCLNTFISQNTLAVFPEMSEVIAQDPIILAGM 914  
QY 252 VKPIYFH 258  
DB 915 VKPLLFH 921

RESULT 14  
PRGR CHICK STANDARD; PRT; 786 AA.

AC P07812; Q90946;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Progesterone receptor (PR).  
GN PGR OR NR3C3.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_Taxid=9031;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8816640; PubMed=3443098;  
RA Gronemeyer H., Turcotte B., Quirin-Sticker C., Bocquet M.T.,  
RA Meyer M.E., Krozowski Z., Jeltsch J.W., Lerouge T., Garnier J.M.,  
RA Chabon P.;  
RT "The chicken progesterone receptor: sequence, expression and  
functional analysis.";  
RL EMBL J. 6:3985-3994(1987).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91042592; PubMed=3153474;  
RA Connely O.M., Dobson A.D.W., Tsai M.-J., Beattie W.G., Toft D.O.,  
RA Huckaby C.S., Zarucki T., Schrader W.T., O'Malley B.W.;  
RT "Sequence and expression of a functional chicken progesterone  
receptor.";  
RL Mol. Endocrinol. 1:517-525(1987).  
RN (3)  
RP SEQUENCE OF 128-164 FROM N.A.  
RX MEDLINE=86289413; PubMed=2426779;  
RA Connely O.M., Sullivan W.P., Toft D.O., Birnhauser M., Cook R.G.,  
RA Maxwell B.L., Zarucki-Schultz T., Greene G.L., Schrader W.T.,  
RA O'Malley B.W.;  
RT "Molecular cloning of the chicken progesterone receptor.";  
RL Science 233:767-770(1986).  
RN (4)  
RP SEQUENCE OF 417-490 FROM N.A.



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9940;

RP SEQUENCE FROM N.A.

RC STRAIN=Romanov; TISSUE=Uterus;

RA Madigou F., Tiffoche C., Le Gal F., Pelletier J., Thieulant M.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

CC -! FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN

CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR

CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

CC -! SUBCELLULAR LOCATION: Nuclear.

CC -! DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,

CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

CC -! SIMILARITY: Belongs to the nuclear hormone receptor family. NR3

CC subfamily.

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CC -----

CC EMBL; 26555; CAA91447.1; -.

DR HSSP; P06401; 1A28.

DR InterPro; IPR000536; Hormone\_rec\_1ig.

DR InterPro; IPR000128; Progester\_receptor.

DR InterPro; IPR001723; Steroidm\_receptor.

DR InterPro; IPR001628; Znf\_C4steroid.

DR Pfam; PF00104; hormone\_rec; 1.

DR Pfam; PF02161; Prog\_receptor; 1.

DR Pfam; PF00105; zf-C4; 1.

DR PRINTS; PR00398; STERHORMONER.

DR PRINTS; PR00047; STEROIDRINGER.

DR PRODOM; PD000035; Znf\_C4steroid; 1.

DR SMART; SM00430; HOL1; 1.

DR SMART; SM00399; Znf\_C4; 1.

DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.

DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;

KW Zinc-finger; Steroid-binding.

FT NON\_TER 1 1

FT DOMAIN <1 15 MODULATING, PRO-RICH.

FT DNA\_BIND 18 83 NUCLEAR RECEPTOR-TYPE.

FT ZN\_RING 18 38 C4-TYPE.

FT ZN\_RING 54 78 C4-TYPE.

FT DOMAIN 128 >377 STEROID-BINDING.

FT NON\_TER 377 377

SO SEQUENCE 377 AA; 42904 MW; 3141B65587F7493C CRC64;

Query Match 53.8%; Score 738; DB 1; Length 377;

Best Local Similarity 55.0%; Pred. No. 1.6e-61;

Matches 133; Conservative 57; Mismatches 52; Indels 0; Gaps 0;

12 PIFLVVLEAIPRGVYAGHNNOPSPFALISINLEIGEROLVHYVKKAKALPGFRNLHV 71

136 PLINLMSIPDVAIVYAGHNSKPTSSLSLTSLNQLGEROLSVYKWSKSLPGFRNLHI 195

72 DDQNAVITYSMGLVPMVGRSFTNVSRLVPAPDLVFNENYRHKSRMYSOCVRMRL 131

196 DDQITLIQYSWMSLMVFGIGRSYKVGSCGLYFAPDLINQRMKSSPSLSCLTMQOI 255

132 SOEGWLTITPQEFLLCKALLPSIIPVDGLKNQKFFDELMMNTYKELDRILIACKRNPT 191

256 PQEFVKLVQVSEEFLLCKVLLNTITPLEGLRSQNFEBMRSYIRBLIKAIIGLRQGVV 315

192 SCNRFPYQLTLDLPVOPIARELHQTFFDLIKSHMVSVDPEPMMAEIIISVQPKIIISGK 251

316 PSSGRFPYQLTLDLPNDLVQQLHLYCLNTRIOSRALSVPEPMMSVYIAQLPKIIIGM 375

252 VK 253

DB 376 VK 377

Search completed: October 9, 2003, 11:41:31  
 Job time: 12 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 9, 2003, 11:40:28 / Search time 19 seconds

(without alignments)  
1315.992 Million cell updates/sec

Title: US-09-687-609A-1

Perfect score: 1371

Sequence: 1 GSHHIEYBRCQPIPLNVLEA.....SVQVPLKLSGKXPIYFHTQ 260

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 76:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349.5	98.4	899	2	A35895 androgen receptor
2	1349.5	98.4	902	2	B40494 androgen receptor
3	1349.5	98.4	919	2	A39248 androgen receptor
4	1341.5	97.8	910	2	A34721 androgen receptor
5	1306	95.3	911	2	B34721 androgen receptor
6	1217	88.8	344	2	I51330 androgen receptor
7	900	65.6	848	2	UG0194 androgen receptor
8	766	55.9	930	2	A25923 progesterone recep
9	765	55.8	933	1	ORHUP progesterone recep
10	759	55.4	923	2	I53280 progesterone recep
11	758	55.3	923	2	A39596 progesterone recep
12	752	54.9	786	2	A35466 progesterone recep
13	665	48.5	984	2	A29513 mineralocorticoid
14	662.5	48.3	777	1	ORHUGA mineralocorticoid
15	662	48.3	981	2	A25691 mineralocorticoid
16	657.5	48.0	783	1	A41401 glucocorticoid rec
17	650.5	47.4	776	1	S44047 glucocorticoid rec
18	648.5	47.3	758	2	S60586 glucocorticoid rec
19	644.5	47.0	771	2	A54273 glucocorticoid rec
20	638.5	46.6	795	1	ORRTG glucocorticoid rec
21	564	41.1	742	1	ORHUGB glucocorticoid rec
22	387	28.2	166	2	S35795 progesterone recep
23	286	20.9	110	2	I53287 progesterone recep
24	222	16.2	535	2	S58224 oestrogen receptor
25	218.5	15.9	589	1	ORCHE oestrogen receptor
26	218	15.9	586	1	ORXLE oestrogen receptor
27	216.5	15.8	595	2	I47140 estradiol receptor
28	215	15.7	620	2	T10423 estrogen receptor
29	214.5	15.6	574	2	A37197 estrogen receptor

## ALIGNMENTS

RESULT 1  
A35895  
androgen receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Oct-1990 #sequence revision 31-Oct-1990 #text change 20-Sep-1999  
C:Accession: A35895; A37255; A37908; S34398; S17198; S40626; I4501; S12082  
R:He, W.W.; Fischer, L.M.; Sun, S.; Bilharz, D.L.; Zhu, X.; Young, C.Y.F.; Kelley, D.B.; Biochem. Biophys. Res. Commun. 171, 697-704, 1990  
A:Title: Molecular cloning of the androgen receptors from divergent species with a polymerase  
epor cDNA probes from dog, guinea pig and clawed frog.  
A:Reference number: A35895; MUID:90386642; PMID:2403358  
A:Accession: A35895  
A:Molecule type: mRNA  
A:Residues: 1-899 <HEA>  
A:Cross-references: EMBL:X53779; NID:949966; PIDN:CAA37795.1; PID:949967  
R:Gaap, M.L.; Mo, T.; Toel, M.  
Mol. Endocrinol. 4, 1600-1610, 1990  
A:Title: Structure and size distribution of the androgen receptor mRNA in wild-type and  
A:Reference number: A37255; MUID:91133435; PMID:2178222  
A:Accession: A37255  
A:Molecule type: mRNA  
A:Status: preliminary  
A:Residues: 1-899 <GAS>  
A:Cross-references: GB:M37890; NID:9191935; PIDN:AA37234.1; PID:9191936  
R:Charest, N.J.; Zhou, Z.; Lubahn, D.B.; Olsen, K.L.; Wilson, E.M.; French, F.S.  
Mol. Endocrinol. 5, 573-581, 1991  
A:Title: A frameshift mutation destabilizes androgen receptor messenger RNA in the Tfm mk  
A:Reference number: A37908; MUID:92017874; PMID:1681426  
A:Accession: A37908  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-899 <CHA>  
A:Cross-references: GB:S56585; NID:9236048; PIDN:AA81916.1; PID:9236049  
R:Feber, P.W.; King, A.; van Rooij, H.C.J.; Brinkmann, A.O.; de Boer, N.J.; Trapman, J.  
Biochem. J. 278, 269-278, 1991  
A:Title: The mouse androgen receptor. Functional analysis of the protein and characteriz  
A:Reference number: S17198; MUID:91354214; PMID:1883356  
A:Accession: S34398  
A:Molecule type: DNA  
A:Residues: 1-899 <FAB>  
A:Cross-references: EMBL:X59592; NID:949968; PIDN:CAA42160.1; PID:949969  
A:Accession: S17198  
A:Molecule type: mRNA  
A:Residues: 1-899 <FA2>  
A:Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969  
R:He, W.W.; Kumar, M.V.; Tindall, D.J.  
Nucleic Acids Res. 19, 2373-2378, 1991  
A:Title: A frame-shift mutation in the androgen receptor gene causes complete androgen it  
A:Reference number: S40626; MUID:91252278; PMID:2041777  
A:Accession: S40626  
A:Status: preliminary  
A:Molecule type: mRNA



A:Residues: 366-413 <HEM>  
 A:Cross-references: EMBL:X53779  
 R:Gaepart, M.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 8606-8610, 1991  
 A:Title: A single base deletion in the Tfm androgen receptor gene creates a short-lived  
 A:Reference number: 149501, MUID:92020902, PMID:1924321  
 A:Accession: 149501  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-899 <RES>  
 A:Cross-references: GB:M37890; NID:g191935; PIDN:AAA37234.1; PID:g191936  
 C:Genetics:  
 A:introns: 518/2; 569/1; 608/1; 704/1; 752/2; 796/1; 848/3  
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
 C:Keywords: DNA binding; transcription regulation; zinc finger  
 F:1-536/Domain: regulatory #status predicted <REG>  
 F:537-795/Domain: erba transforming protein homology <ERBA>  
 F:539-559/Region: zinc finger  
 F:575-599/Region: zinc finger  
 F:650-899/Domain: hormone binding #status predicted <LIG>

Query Match 98.4%; Score 1349.5; DB 2; Length 899;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-118;

Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGYCOPIFLNVLAIIEPGVVCAGHDNNDPDSFALLSSINELGEROLVHVYKAK 61  
 DB 642 SH-IEGYCOPIFLNVLAIIEPGVVCAGHDNNDPDSFALLSSINELGEROLVHVYKAK 700  
 QY 62 ALPGFNNLHVDQMAVIOYSWNGLVFAMGWRSTFNVSRLMYPADLVFNEYRMHKSRLM 121  
 DB 701 ALPGFNNLHVDQMAVIOYSWNGLVFAMGWRSTFNVSRLMYPADLVFNEYRMHKSRLM 760  
 QY 122 YSQCVMRHLISOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFPELNMNYIKELDR 181  
 DB 761 YSQCVMRHLISOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFPELNMNYIKELDR 820  
 QY 182 IIAKCKKNPTSCSRFFYQLTKLDSVQPIARELHQTFTDLLIKSHMVSVDPEPMAAIIIS 241  
 DB 821 IIAKCKKNPTSCSRFFYQLTKLDSVQPIARELHQTFTDLLIKSHMVSVDPEPMAAIIIS 880  
 QY 242 VQVFKILSGKVPYFHTQ 260  
 DB 881 VQVFKILSGKVPYFHTQ 899

# RESULT 2

B40494  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #text change 20-Sep-1999  
 C:Accession: B40494; A34943; A36283; B40108  
 R:Chang, C.; Kokontis, J.; Liao, S.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988  
 A:Title: Structural analysis of complementary DNA and amino acid sequences of human and  
 A:Reference number: A40494; MUID:89017168; PMID:3174628  
 A:Accession: B40494  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-902 <CHA>  
 A:Cross-references: GB:M23264; NID:g202967; PIDN:AAA40759.1; PID:g202968  
 R:Tan, J.; Joseph, D.R.; Quarby, V.E.; Lubahn, D.B.; Sar, M.; French, F.S.; Wilson, E.M.  
 Mol. Endocrinol. 2, 1276-1285, 1988  
 A:Title: The rat androgen receptor: primary structure, autoregulation of its messenger  
 A:Reference number: A34943; MUID:89112209; PMID:3216867  
 A:Accession: A34943  
 A:Molecule type: mRNA  
 A:Residues: 1-388 'S', 390-902 <TAN>  
 A:Cross-references: GB:M20133; NID:g202895; PIDN:AAA40733.1; PID:g202896  
 R:Fairbrough, W.G.; Quarby, V.E.; Simental, J.A.; Joseph, D.R.; Sar, M.; Lubahn, D.B.; C  
 J. Biol. Chem. 265, 8893-8900, 1990  
 A:Title: A single base mutation in the androgen receptor gene causes androgen insensitivity  
 A:Reference number: A36283; MUID:90256822; PMID:2341409

A:Accession: A36283  
 A:Molecule type: mRNA  
 A:Residues: 1-194, 196-902 <YAR>  
 A:Cross-references: GB:J05454  
 R:Chang, C.; Kokontis, J.; Liao, S.  
 Science 240, 324-326, 1988  
 A:Title: Molecular cloning of human and rat complementary DNA encoding androgen receptor  
 A:Reference number: A40108; MUID:88178111; PMID:3353726  
 A:Accession: B40108  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 540-611 <CH2>  
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
 C:Keywords: DNA binding; zinc finger  
 F:540-798/Domain: erba transforming protein homology <ERBA>  
 F:542-562/Region: zinc finger  
 F:578-602/Region: zinc finger

Query Match 98.4%; Score 1349.5; DB 2; Length 902;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-118;

Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGYCOPIFLNVLAIIEPGVVCAGHDNNDPDSFALLSSINELGEROLVHVYKAK 61  
 DB 645 SH-IEGYCOPIFLNVLAIIEPGVVCAGHDNNDPDSFALLSSINELGEROLVHVYKAK 703  
 QY 62 ALPGFNNLHVDQMAVIOYSWNGLVFAMGWRSTFNVSRLMYPADLVFNEYRMHKSRLM 121  
 DB 704 ALPGFNNLHVDQMAVIOYSWNGLVFAMGWRSTFNVSRLMYPADLVFNEYRMHKSRLM 763  
 QY 122 YSQCVMRHLISOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFPELNMNYIKELDR 181  
 DB 764 YSQCVMRHLISOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFPELNMNYIKELDR 823  
 QY 182 IIAKCKKNPTSCSRFFYQLTKLDSVQPIARELHQTFTDLLIKSHMVSVDPEPMAAIIIS 241  
 DB 824 IIAKCKKNPTSCSRFFYQLTKLDSVQPIARELHQTFTDLLIKSHMVSVDPEPMAAIIIS 883  
 QY 242 VQVFKILSGKVPYFHTQ 260  
 DB 884 VQVFKILSGKVPYFHTQ 902

# RESULT 3

A39248  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Oct-1991 #sequence revision 04-Oct-1991 #text change 24-Nov-1999  
 C:Accession: A39248; A30328; A60946; A34942; A27653; A40108; A40494; A32224; A40  
 R:Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgs, H.N.; Wilson, C.J.; Wilson, E.M.; Fr  
 Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989  
 A:Title: Sequence of the intron/exon junctions of the coding region of the human androge  
 A:Reference number: A39248; MUID:90083302; PMID:2594783  
 A:Accession: A39248  
 A:Molecule type: DNA  
 A:Residues: 1-919 <LUB>  
 A:Cross-references: GB:M27423; GB:M27430; NID:g178904; PIDN:AAA51886.1; PID:g178906  
 R:Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; Van der Korput, J.A.G.M.; Brinkmann,  
 Mol. Cell. Endocrinol. 61, 257-262, 1989  
 A:Title: The N-terminal domain of the human androgen receptor is encoded by one, large e  
 A:Reference number: A30328; MUID:89137730; PMID:2917688  
 A:Accession: A30328  
 A:Molecule type: DNA  
 A:Residues: 1-77, 79-165, 'A', 167-389, 'L', 391-464, 473-538 <FAB>  
 A:Cross-references: GB:M20260  
 R:Lubahn, D.B.; Joseph, D.R.; Sullivan, P.M.; Willard, H.F.; French, F.S.; Wilson, E.M.  
 Science 240, 327-330, 1988  
 A:Title: Cloning of human androgen receptor complementary DNA and localization to the X  
 A:Reference number: A40109; MUID:88178112; PMID:3353727  
 A:Accession: A40109  
 A:Molecule type: DNA  
 A:Residues: 559-624 <LUB>  
 A:Cross-references: GB:M20132



R.Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.C.J.; van der Korp, J.A.G.M.; Ris-Stalpe J. Mol. Endocrinol. 2, R1-R4, 1989  
 A>Title: Structural organization of the human androgen receptor gene.  
 A.Reference number: A60946; PMID:89322749; PMID:2546571  
 A.Accession: A60946  
 A.Molecule type: DNA  
 A.Residues: 536-540;587-591;626-631;723-726;770-774;814-818;867-870 <RUI>  
 R.Lubahn, D.B.; Joseph, D.R.; Sax, M.; Tan, J.; Hsige, H.N.; Larson, R.E.; French, F.S.; Mol. Endocrinol. 2, 1265-1275, 1988  
 A>Title: The human androgen receptor: complementary deoxyribonucleic acid cloning, sequence and expression.  
 A.Reference number: A34942; PMID:89112208; PMID:3216866  
 A.Accession: A34942  
 A.Molecule type: mRNA  
 A.Residues: 1-919 <RUI>  
 A.Cross-references: GB:M20132; NID:g178627; PIDN:AA51729.1; PID:g178628; GB:J03180  
 R.Trapman, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korp, J.A.G.M.; Faber, P.W.; van Bloemen, Biophys. Res. Commun. 153, 241-248, 1988  
 A>Title: Cloning, structure and expression of a cDNA encoding the human androgen receptor.  
 A.Reference number: A27653; PMID:88240407; PMID:3377788  
 A.Accession: A27653  
 A.Molecule type: mRNA  
 A.Residues: 468-564, 'K', 566-919 <TRA>  
 A.Cross-references: GB:M20260; NID:g178891; PIDN:AA51774.1; PID:g178892  
 A>Note: The authors translated the codon AAG for residue 565 as Glu  
 R.Chang, C.; Kokontis, J.; Liao, S. Science 240, 324-326, 1988  
 A>Title: Molecular cloning of human and rat complementary DNA encoding androgen receptor.  
 A.Reference number: A40108; PMID:88178111; PMID:3353726  
 A.Accession: A40108  
 A.Molecule type: mRNA  
 A.Residues: 557-628 <CHA>  
 A.Cross-references: GB:M18624  
 R.Chang, C.; Kokontis, J.; Liao, S. Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988  
 A>Title: Structural analysis of complementary DNA and amino acid sequences of human and rat androgen receptor.  
 A.Reference number: A40494; PMID:89017168; PMID:3174628  
 A.Accession: A40494  
 A.Molecule type: mRNA  
 A.Residues: 1-74, 79-89, 'H', 90-472, 'GGG', 473-474, 'E', 476-644, 'N', 646-919 <CH2>  
 A.Cross-references: GB:M23263  
 R.Tilley, W.D.; MacNeill, M.; Wilson, J.D.; McPhaul, M.J. Proc. Natl. Acad. Sci. U.S.A. 86, 337-331, 1989  
 A>Title: Characterization and expression of a cDNA encoding the human androgen receptor.  
 A.Reference number: A32224; PMID:89098999; PMID:29151578  
 A.Accession: A32224  
 A.Molecule type: mRNA  
 A.Residues: 1-77, 79-211, 'R', 213-471, 473-919 <TIL>  
 A.Cross-references: GB:M21748; GB:J04150; NID:g178871; PIDN:AA51771.1; PID:g178872  
 R.Mowzowicz, I.; Lee, H.J.; Chen, H.T.; Westayer, C.; Porcels, M.C.; Cabrol, S.; Mauvaud Mol. Endocrinol. 7, 861-869, 1993  
 A>Title: A point mutation in the second zinc finger of the DNA-binding domain of the androgen receptor.  
 A.Reference number: A40715; PMID:94019395; PMID:8413310  
 A.Accession: A40715  
 A>Status: not compared with conceptual translation  
 A.Molecule type: DNA  
 A.Residues: 557-614, 'H', 616-624 <MOW>  
 A.Cross-references: PIDN:AA828340.1; PID:9425580  
 A.Accession: A40715  
 A.Gene: GDB:AR  
 A.Cross-references: GDB:120556; OMIM:313700  
 A.Map position: Xq11-Xq12  
 A.Introns: 538/2; 589/1; 628/1; 724/1; 772/2; 816/1; 868/3  
 C:Superfamily: unassigned exba-related proteins; exba transforming protein homology  
 C:Keywords: DNA binding; steroid binding; transcription regulation; zinc finger  
 F:557-815/Domain: exba transforming protein homology <ERBA>  
 F:559-579/Region: zinc finger  
 F:595-619/Region: zinc finger

Query Match 98.4%; Score 1349.5; DB 2; Length 919;  
 Best Local Similarity 99.6%; Pred. No. 2, 6e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 97.8%; Score 1341.5; DB 2; Length 910;  
 Best Local Similarity 98.8%; Pred. No. 1, 4e-117;  
 Matches 256; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Query Match 98.4%; Score 1349.5; DB 2; Length 919;  
 Best Local Similarity 99.6%; Pred. No. 2, 6e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

A:Title: Specific region in hormone binding domain is essential for hormone binding and  
 A:Reference number: A34721; MUID:90258935; PMID:2342476  
 A:Accession: B34721  
 A:Molecule type: mRNA  
 A:Residues: 1-911 <GO2>  
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
 C:Keywords: zinc finger  
 F:548-806/Domain: erba transforming protein homology <ERBA>  
 F:550-570/Region: zinc finger  
 F:586-610/Region: zinc finger

Query Match 95.3%; Score 1306; DB 2; Length 911;  
 Best Local Similarity 97.3%; Pred. No. 3.1e-114;  
 Matches 253; Conservative 1; Mismatches 4; Indels 2; Gaps 2;

QY 2 SHMIEGECOPFLNVLNLEIEPGVCAAGHDNNDPSFALLSLNLSLGEROLVHYVYKAKALP 61  
 DB 653 SH-IEGECOPFLNVLNLEIEPGVCAAGHDNNDPSFALLSLNLSLGEROLVHYVYKAKALP 711  
 QY 62 ALPGFRLNLDVDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 121  
 DB 712 ALPGFRLNLDVDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 771  
 QY 122 YSGCVRMRHLSQBFGLQITPQFLCMKALLFSIIPVGLKNQ-KFPELDMNYIKELD 180  
 DB 772 YSGCVRMRHLSQBFGLQITPQFLCMKALLFSIIPVGLKNQIFFFFLNNYIKELD 831  
 QY 181 RIIACKRKNPSCSRRFQYLTKLDSVQPIARELHOFEDLLIKSHMVSVDPEMMAEII 240  
 DB 832 RIIACKRKNPSCSRRFQYLTKLDSVQPIARELHOFEDLLIKSHMVSVDPEMMAEII 891  
 QY 241 SVQVPEKILSGKVPYFHTQ 260  
 DB 892 SVQVPEKILSGKVPYFHTQ 911

## RESULT 6

151330  
 androgen receptor - common canary (fragment)  
 C:Species: Serinus canaria (common canary)  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 20-Sep-1999  
 C:Accession: I51330  
 R:Nastjuk, K.L.; Clayton, D.F.  
 Endocrinology 134, 640-649, 1994  
 A:Title: Seasonal and tissue-specific regulation of canary androgen receptor messenger  
 A:Reference number: I51330; MUID:94130808; PMID:8299561  
 A:Accession: I51330  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <NMS>  
 A:Cross-references: GB:L25901; NID:9414733; PIDN:AAA17402.1; PID:9414734  
 C:Genetics:  
 A:Gene: AR  
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
 C:Keywords: zinc finger  
 F:1-251/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match 88.8%; Score 1217; DB 2; Length 344;  
 Best Local Similarity 92.7%; Pred. No. 2e-106;  
 Matches 227; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY 5 IEIEGECOPFLNVLNLEIEPGVCAAGHDNNDPSFALLSLNLSLGEROLVHYVYKAKALP 64  
 DB 100 IDIEGECOPFLNVLNLEIEPGVCAAGHDNNDPSFALLSLNLSLGEROLVHYVYKAKALP 159  
 QY 65 GFRLNLDVDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 124  
 DB 160 GFRLNLDVDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 219  
 QY 125 CVMRHLISQBFGLQITPQFLCMKALLFSIIPVGLKNQKFPELDMNYIKELDRITA 184  
 DB 220 CVMRHLISQBFGLQITPQFLCMKALLFSIIPVGLKNQKFPELDMNYIKELDRITA 279

QY 185 CKRKNPSCSRRFQYLTKLDSVQPIARELHOFEDLLIKSHMVSVDPEMMAEIIISVOV 244  
 DB 280 CKRKNPSCSRRFQYLTKLDSVQPIARELHOFEDLLIKSHMVSVDPEMMAEIIISVOV 339  
 QY 245 PKILS 249  
 DB 340 PKILS 344

## RESULT 7

androgen receptor - Japanese eel  
 C:Species: Anguilla japonica (Japanese eel)  
 C>Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 11-May-2000  
 C:Accession: JG0194  
 R:Todo, T.; Ikeuchi, T.; Kobayashi, T.; Nagahama, Y.  
 Biochem. Biophys. Res. Commun. 254, 378-383, 1999  
 A:Title: Fish androgen receptor: cDNA cloning, steroid activation of transcription in tri  
 A:Reference number: JG0194; MUID:99119319; PMID:9918846  
 A:Accession: JG0194  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-848 <TOD>  
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
 F:491-745/Domain: erba transforming protein homology <ERB>

Query Match 65.6%; Score 900; DB 2; Length 848;  
 Best Local Similarity 68.1%; Pred. No. 3.7e-76;  
 Matches 173; Conservative 35; Mismatches 42; Indels 4; Gaps 2;

QY 7 GYECOPFLNVLNLEIEPGVCAAGHDNNDPSFALLSLNLSLGEROLVHYVYKAKALPGF 66  
 DB 596 GFHTQSMFLNLEIEPGVCAAGHDNNDPSFALLSLNLSLGEROLVHYVYKAKALPGF 655  
 QY 67 RNLHVDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 126  
 DB 656 RSLVYDDQMAVIOYSWGLMVFAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 715  
 QY 127 RMRHLSQBFGLQITPQFLCMKALLFSIIPVGLKNQKFPELDMNYIKELDRITA 186  
 DB 716 RMRHLSQBFGLQITPQFLCMKALLFSIIPVGLKNQKFPELDMNYIKELDRITA 775  
 QY 187 RKNPSCSRRFQYLTKLDSVQPIARELHOFEDLLIKSHMVSVDPEMMAEIIISVOV 244  
 DB 776 SK--SSGSRKQQLRLDSVQPIARELHOFEDLLIKSHMVSVDPEMMAEIIISVOV 833  
 QY 245 PKILSGKVPYFHTQ 258  
 DB 834 PKILSGKVPYFHTQ 847

## RESULT 8

A25923  
 progesterone receptor - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 20-Aug-1999  
 C:Accession: A25923  
 R:Loosfelt, H.; Atger, M.; Mistrati, M.; Gulochon-Mantel, A.; Meriel, C.; Logeat, F.; Ben  
 Proc. Natl. Acad. Sci. U.S.A. 83, 9045-9049, 1986  
 A:Title: Cloning and sequence analysis of rabbit progesterone-receptor complementary DNA  
 A:Reference number: A25923; MUID:87067449; PMID:3558016  
 A:Accession: A25923  
 A:Molecule type: mRNA  
 A:Residues: 1-930 <LOO>  
 A:Cross-references: GB:M14547; NID:9165631; PIDN:AAA31443.1; PID:9165632  
 C:Superfamily: progesterone receptor; erba transforming protein homology  
 C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi  
 F:566-826/Domain: erba transforming protein homology <ERBA>  
 F:568-588/Region: zinc finger  
 F:604-628/Region: zinc finger

Query Match 55.9%; Score 766; DB 2; Length 930;  
 Best Local Similarity 55.5%; Pred. No. 1.6e-63;





QY 12 PFLNVLNLAIBGVVACAGHNNQDPSFALLSLNLSLGERQVHVYKAKALPGFNNLHV 71  
 Db PFMISVLNGIBPEVYVAGYDNNKPNPSSLSLNLHLCERQQLCVYKSKLLPGFNNLHV 597  
 QY 72 DDQNAVIOYSWGLMVPFAMGWSFTNVNSRLYPADLVFNENYKHSRMSYQCYRMHL 131  
 Db DDQNAVIOYSWGLMVPFAMGWSFTNVNSRLYPADLVFNENYKHSRMSYQCYRMHL 598  
 QY 132 SOEFGMLITPOEPLCMKALLFSIIIPVDGLKNOKFPEDELMNXYIKELDRITACRKNPT 191  
 Db POEFGMLITPOEPLCMKALLFSIIIPVDGLKNOKFPEDELMNXYIKELDRITACRKNPT 658  
 QY 192 SCRRFVYLTKLDSVQPIARELHOFTEPDLIKSHVSVDPPEMAAIIISVQPKILSGK 251  
 Db ANSGFVYLTKLDSVQPIARELHOFTEPDLIKSHVSVDPPEMAAIIISVQPKILSGK 778  
 QY 252 VKPIYFH 258  
 Db VKPIYFH 784

## RESULT 13

A29513  
 A:Accession: A29513  
 A:Title: mineralocorticoid receptor - human  
 N:Alternate names: aldosterone receptor  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 20-Sep-1999  
 C/Accession: A29513  
 A:Title: Cloning of human mineralocorticoid receptor complementary DNA: structural and  
 A:Reference number: A29513; MUID:87263386; PMID:3037703  
 A:Accession: A29513  
 A:Molecule type: mRNA  
 A:Residues: 1-384 <ARK>  
 A:Cross-references: GB:M16801; NID:G187460; PIDN:AAA59571.1; PID:G307166  
 C/Genetics:  
 A:Gene: GDB:MLR  
 A:Cross-references: GDB:120188; OMIM:264350  
 A:Map position: 4q31-4q31  
 C/Superfamily: unassigned erba-related proteins; erba transforming protein homology  
 C/Keywords: DNA binding; transcription regulation; zinc finger  
 F:601-880/Domain: erba transforming protein homology <ERBA>  
 F:603-623/Region: zinc finger  
 F:639-663/Region: zinc finger

Query Match 48.5%; Score 665; DB 2; Length 984;  
 Best Local Similarity 52.9%; Pred. No. 5.2e-54;  
 Matches 128; Conservative 44; Mismatches 70; Indels 0; Gaps 0;

QY 17 VLEAIEBPVVCAGHNNQDPSFALLSLNLSLGERQVHVYKAKALPGFNNLHVDDQMA 76  
 Db VLEAIEBPVVCAGHNNQDPSFALLSLNLSLGERQVHVYKAKALPGFNNLHVDDQMA 741  
 QY 77 VIOYSWGLMVPFAMGWSFTNVNSRLYPADLVFNENYKHSRMSYQCYRMHLISQF 136  
 Db VIOYSWGLMVPFAMGWSFTNVNSRLYPADLVFNENYKHSRMSYQCYRMHLISQF 801  
 QY 137 WLQITPOEFLCMKALLFSIIIPVDGLKNOKFPEDELMNXYIKELDRITACRKNPTSCRR 196  
 Db WLQITPOEFLCMKALLFSIIIPVDGLKNOKFPEDELMNXYIKELDRITACRKNPTSCRR 861  
 QY 197 FYQVLTKLDSVQPIARELHOFTEPDLIKSHVSVDPPEMAAIIISVQPKILSGKVPY 256  
 Db FYQVLTKLDSVQPIARELHOFTEPDLIKSHVSVDPPEMAAIIISVQPKILSGKVPY 920  
 QY 257 FH 258  
 Db FH 982

## RESULT 14

## ORHUGA

glucocorticoid receptor, alpha splice form - human  
 N:Alternate names: hGR  
 C/Species: Homo sapiens (man)  
 C/Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 21-Jul-2000  
 C/Accession: A93370; A39837; A39779; I56596; A03246; A32186  
 R:Hollenberg, S.M.; Weinberger, C.; Ong, E.S.; Cerelli, G.; Oro, A.; Lebo, R.; Thompson, N.  
 Nature 318, 635-641, 1985  
 A:Title: Primary structure and expression of a functional human glucocorticoid receptor  
 A:Reference number: A93370; MUID:86092206; PMID:2867473  
 A:Accession: A93370  
 A:Molecule type: mRNA  
 A:Residues: 1-777 <HOL>  
 A:Cross-references: EMBL:X03225; GB:M10901; NID:G31679; PIDN:CAA26976.1; PID:G31680  
 R:Leclerc, S.; Xie, B.; Roy, R.; Govindan, M.V.  
 J. Biol. Chem. 266, 8711-8719, 1991  
 A:Title: Purification of a human glucocorticoid receptor gene promoter-binding protein.  
 A:Reference number: A39837; MUID:91224961; PMID:2026589  
 A:Accession: A39837  
 A:Molecule type: DNA  
 A:Residues: 1-394 <LEC>  
 A:Cross-references: GB:M69104; NID:G183605; PIDN:AAA8049.1; PID:G553322  
 R:Encio, I.J.; Delella-Wadleigh, S.D.  
 J. Biol. Chem. 266, 7182-7188, 1991  
 A:Title: The genomic structure of the human glucocorticoid receptor.  
 A:Reference number: A39779; MUID:91201378; PMID:1707881  
 A:Accession: A39779  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 385-404; A41-459; A480-498; 573-593; 621-640; 665-685; 718-737 <ENC>  
 A:Cross-references: GB:M60597  
 A:Experimental source: placenta  
 R:Weinberger, C.; Hollenberg, S.M.; Rosenfeld, M.G.; Evans, R.M.  
 Nature 318, 670-672, 1985  
 A:Title: Domain structure of human glucocorticoid receptor and its relationship to the v-  
 A:Reference number: A93373; MUID:86092211; PMID:3841189  
 A:Contents: annotation; domain  
 R:Dahlman, K.; Stromstedt, P.E.; Rae, C.; Joernvall, H.; Floock, J.I.; Carlstedt-Duke, J.  
 J. Biol. Chem. 264, 804-809, 1989  
 A:Title: High level expression in *Escherichia coli* of the DNA-binding domain of the glucocorticoid receptor  
 A:Reference number: A32196; MUID:89093147; PMID:2642905  
 A:Contents: annotation; domain  
 A:Note: engineered sequence expressed in *Escherichia coli*  
 R:Govindan, M.V.; Pochier, P.; Leclerc, S.; Palaniswami, R.; Xie, B.  
 J. Steroid Biochem. Mol. Biol. 40, 317-323, 1991  
 A:Title: Human glucocorticoid receptor gene promoter-homologous down regulation.  
 A:Reference number: I56596; MUID:92068829; PMID:1958537  
 A:Accession: I56596  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-394 <RES>  
 A:Cross-references: GB:M68378; NID:G239757; PIDN:AA20466.1; PID:G239758  
 C/Comment: Alpha and beta (see PIR:Q8UGB) splice forms differ in their carboxyl-terminal  
 C/Genetics:  
 A:Gene: GDB:GRL  
 A:Cross-references: GDB:120017; OMIM:138040  
 A:Map position: 5q31-5q31  
 A:Initons: 395/2; 451/1; 490/1; 583/1; 631/2; 675/1; 727/3  
 A:Note: the first intron occurs before the initiator codon  
 C/Superfamily: glucocorticoid receptor; erba transforming protein homology  
 C/Keywords: alternative splicing; DNA binding; nucleus; steroid hormone receptor; transci  
 F:419-674/Domain: erba transforming protein homology <ERBA>  
 F:421-441/Region: zinc finger CCCC motif  
 F:457-481/Region: zinc finger CCCC motif  
 F:728-777/Domain: steroid binding #status predicted <STB>

Query Match 48.3%; Score 662.5; DB 1; Length 777;  
 Best Local Similarity 50.6%; Pred. No. 6.5e-54;  
 Matches 125; Conservative 49; Mismatches 72; Indels 1; Gaps 1;

QY 12 PFLNVLNLAIBGVVACAGHNNQDPSFALLSLNLSLGERQVHVYKAKALPGFNNLHV 71  
 Db PFLNVLNLAIBGVVACAGHNNQDPSFALLSLNLSLGERQVHVYKAKALPGFNNLHV 530

```
QY 72 DDQNAVIOYSWGLMVFAMGRSFTNNSRLVFPADLVFENEYRHKSRMYSQCVRMHL 131
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 590 DDQNTLQYSWVFLWAFALGWRSSYRQSSANILCFAPDLIINEQRMTLPCMTDQCKEMLYV 649
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 132 SOBERMLOITPOEFLCMKALLFSIIPVDGLNOKFPDELPMNYIKELDRITACKRKNET 191
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 650 SSELHRLQVSYEELCMKTLTLLSSVPRDGLKSQELPDIRMTYIKELGKALVKREGNS 709
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 192 SCSRRFYOLTLLDSDVOPARELHOFTFDLTKSHMVSVDPEMMAEIIISVQPKILSGK 251
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 710 QMWQRFYOLTLLDSDMHEVENLAVCFOTPLDKTM-SIRPEPMLEIITITNOIPKXSGN 768
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 252 VKPIYFH 258
    |||:|||||
Db 769 IKKLIFH 775
    |||:|||||
```

## RESULT 15

```
A1401
mineralocorticoid receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 20-Sep-1999
C:Accession: A1401
R:Patel, P.D.; Sherman, T.G.; Goldman, D.J.; Watson, S.J.
Mol. Endocrinol. 3, 1877-1885, 1989
A:Title: Molecular cloning of a mineralocorticoid (type I) receptor complementary DNA fr
A:Reference number: A1401; MUID:90114194; PMID:2558305
A:Accession: A1401
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-981 <P>A>
A:Cross-references: GB:M36074; NID:9205340; PIDN:AAA1583.1; PID:9205341
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger
F:602-877/Domain: erba transforming protein homology <ERBA>
F:604-624/Region: zinc finger
F:640-664/Region: zinc finger
```

Query Match 48.3%; Score 662; DB 2; Length 981;

Best Local Similarity 52.2%; Pred. No. 9, 9e-54;

Matches 128; Conservative 47; Mismatches 64; Indels 6; Gaps 2;

```
QY 17 VLEALBPQVCAQHNNPDSPALISSINELGERQLVHVTKAKALPGRNLIHVDQMA 76
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 738 ILENIEPEVTVAGYNSKEDTAESLSTINRLAAKOMIQVWAKVLPFGKMLPLEDQIT 797
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 77 VIOYSMMGLMVFAMGRSFTNNSRLVFPADLVFENEYRHKSRMYSQCVRMHL 136
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 798 LIQYSMMCLSSPALSFKHTNSQLVFPADLVFENEYRHKSRMYSQCVRMHL 857
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 137 WLOITPOEFLCMKALLFSIIPVDGLNOKFPDELPMNYIKELDRITACKRKNET 194
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 858 RQLTFEEXSINKVLLSTVPRDGLKSQAAPFEMRTNYIKELRKVLT--KCPNSSGQS 914
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 195 -RRFTQLTLLDSDVOPARELHOFTFDLTKSHMVSVDPEMMAEIIISVQPKILSGK 253
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 915 WQRFYOLTLLDSDMHEVENLAVCFOTPLDKTM-SIRPEPMLEIITITNOIPKXSGN 974
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 254 PIYFH 258
    |||:|||||
Db 975 PIYFH 979
    |||:|||||
```

Search completed: October 9, 2003, 11:43:05  
Job time : 20 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 11:41:18 ; Search time 27 Seconds  
(without alignments)  
1551.607 Million cell updates/sec

Title: US-09-687-609A-1  
Perfect score: 1371  
Sequence: 1 GSHMIEGECQPIFLNVLRA.....SVQPKLSGKPKYFHTQ 260

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

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7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1349.5	98.4	263	US-10-220-981-1	Sequence 1, Appl1
2	1349.5	98.4	388	US-09-997-267-2	Sequence 2, Appl1
3	1349.5	98.4	907	US-10-008-739A-2	Sequence 2, Appl1
4	1349.5	98.4	919	US-10-205-823-36	Sequence 36, Appl1
5	1243	90.7	246	US-09-885-827-1	Sequence 1, Appl1
6	813.5	59.3	294	US-09-997-267-4	Sequence 1, Appl1
7	765	55.8	258	US-10-220-981-3	Sequence 3, Appl1
8	765	55.8	314	US-09-887-280-4	Sequence 4, Appl1
9	765	55.8	933	US-10-207-655-63	Sequence 63, Appl1
10	728	53.1	240	US-09-905-176-13	Sequence 11, Appl1
11	666	48.6	215	US-09-905-176-11	Sequence 13, Appl1
12	662.5	48.3	777	US-10-153-668-226	Sequence 226, Appl1
13	662	48.3	689	US-10-202-846B-2	Sequence 2, Appl1
14	639.5	46.6	1070	US-10-001-486B-2	Sequence 2, Appl1
15	630.5	46.0	284	US-09-853-450-20	Sequence 20, Appl1

16	224	16.3	1099	US-10-259-864-4	Sequence 4, Appl1
17	218	15.9	49	US-10-153-398-12	Sequence 12, Appl1
18	217	15.8	595	US-10-437-107-30	Sequence 30, Appl1
19	217	15.8	595	US-10-052-092-30	Sequence 30, Appl1
20	216.5	15.8	595	US-10-437-107-31	Sequence 31, Appl1
21	216.5	15.8	595	US-10-052-092-31	Sequence 31, Appl1
22	215	15.7	595	US-09-893-666A-2	Sequence 2, Appl1
23	213.5	15.6	323	US-09-737-255-5	Sequence 5, Appl1
24	213.5	15.6	910	US-09-908-153B-40	Sequence 40, Appl1
25	213.5	15.6	922	US-09-908-153B-42	Sequence 42, Appl1
26	211.5	15.4	596	US-10-278-481-16	Sequence 16, Appl1
27	209	15.2	460	US-10-295-370-4	Sequence 4, Appl1
28	209	15.2	460	US-10-292-356-4	Sequence 4, Appl1
29	209	15.2	460	US-10-292-324-4	Sequence 4, Appl1
30	208.5	15.2	660	US-09-853-033-4	Sequence 4, Appl1
31	207.5	15.1	414	US-10-157-899A-2	Sequence 2, Appl1
32	207.5	15.1	414	US-10-157-899A-6	Sequence 6, Appl1
33	207.5	15.1	414	US-10-157-899A-10	Sequence 10, Appl1
34	207.5	15.1	438	US-10-157-899A-4	Sequence 4, Appl1
35	207.5	15.1	438	US-10-157-899A-12	Sequence 12, Appl1
36	207.5	15.1	438	US-10-157-899A-16	Sequence 16, Appl1
37	207.5	15.1	472	US-09-965-703-61	Sequence 61, Appl1
38	207.5	15.1	595	US-09-853-033-2	Sequence 2, Appl1
39	207.5	15.1	660	US-09-853-033-8	Sequence 8, Appl1
40	206.5	15.1	241	US-09-905-176-14	Sequence 14, Appl1
41	206.5	15.1	484	US-10-278-481-13	Sequence 13, Appl1
42	206.5	15.1	485	US-10-278-481-2	Sequence 2, Appl1
43	206	15.0	511	US-10-006-760-19	Sequence 19, Appl1
44	204.5	14.9	243	US-09-903-876-1	Sequence 1, Appl1
45	204.5	14.9	414	US-10-157-899A-8	Sequence 8, Appl1

#### ALIGNMENTS

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RESULT 1
US-10-220-981-1
; Sequence 1, Application US/10220981
; Publication No. US20030167999A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; APPLICANT: Donner, Peter
; APPLICANT: Egner, Ursula
; APPLICANT: Carrondo, Maria A
; APPLICANT: Matias, Pedro M
; TITLE OF INVENTION: Crystall
; FILE REFERENCE: P008463WO CTH
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: GB 0005689.5
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 263
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-220-981-1
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QY	2	SHMIEGECQPIFLNVLRAIEPGVVCAGHNNQPSFALLSLNLSLGEROLVHVVKAK	61
DB	6	SH-IEIEYECQPIFLNVLRAIEPGVVCAGHNNQPSFALLSLNLSLGEROLVHVVKAK	64
QY	62	ALPGFNHLVDDQMAVIOYSNMGIMVAFMGKRSFTNVNSRMTYFAPDLVFNERYMKSRM	121
DB	65	ALPGFNHLVDDQMAVIOYSNMGIMVAFMGKRSFTNVNSRMTYFAPDLVFNERYMKSRM	124
QY	122	YSQCVARHLSQEFQWLTTPQFLCMKALLFSIIPVGLNKKQFDELRMNYIKELDR	181



Db 125 YSQCVRMRHLSQBFQWLTQTPQEFLLCMKALLFSIIPVGLKQKQFDELMNYIKELDR 184  
QY 182 IIAKCKRNPFTSCSRFFQTLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMMARITIS 241  
Db 185 IIAKCKRNPFTSCSRFFQTLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMMARITIS 244  
QY 242 VQVFKILSGKVKPIYFHTQ 260  
Db 245 VQVFKILSGKVKPIYFHTQ 263

## RESULT 2

US-09-97-267-2  
Sequence 2, Application US/09997267  
Patent No. US2002016381A1  
GENERAL INFORMATION:  
APPLICANT: AHRENS-FATH, ISABELLE  
APPLICANT: HAENDLER, BERNARD  
TITLE OF INVENTION: HUMAN ANDROGEN RECEPTOR VARIANTS  
FILE REFERENCE: SCH-1793  
CURRENT APPLICATION NUMBER: US/09/997,267  
CURRENT FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 60/255,078  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 388  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-97-267-2

Query Match 98.4%; Score 1349.5; DB 10; Length 388;  
Best Local Similarity 99.6%; Pred. No. 2e-142;  
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 2 SHMIEGYECOPIFLNTVLEAIEPVGVCAGHDNNOPDSFALLSSINELGERRQLVHVMKAK 61  
Db 131 SH-IEGYECOPIFLNTVLEAIEPVGVCAGHDNNOPDSFALLSSINELGERRQLVHVMKAK 189  
QY 62 ALPFRNLHVDDQNAVIOYSWGLMVFAMGWRSPFTNVSRMLYFAPDLVFNERYMHSRM 121  
Db 190 ALPFRNLHVDDQNAVIOYSWGLMVFAMGWRSPFTNVSRMLYFAPDLVFNERYMHSRM 249  
QY 122 YSQCVRMRHLSQBFQWLTQTPQEFLLCMKALLFSIIPVGLKQKQFDELMNYIKELDR 181  
Db 250 YSQCVRMRHLSQBFQWLTQTPQEFLLCMKALLFSIIPVGLKQKQFDELMNYIKELDR 309  
QY 182 IIAKCKRNPFTSCSRFFQTLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMMARITIS 241  
Db 310 IIAKCKRNPFTSCSRFFQTLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMMARITIS 369  
QY 242 VQVFKILSGKVKPIYFHTQ 260  
Db 370 VQVFKILSGKVKPIYFHTQ 388

## RESULT 3

US-10-008-739A-2  
Sequence 2, Application US/10008739A  
Publication No. US20020161194A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Inc.  
APPLICANT: Castleberry, Teessa A.  
APPLICANT: Lu, Bihong  
APPLICANT: Owen, Steven A.  
APPLICANT: Smock, Steven L.  
TITLE OF INVENTION: The Canine Androgen Receptor  
FILE REFERENCE: PCI0893JAGR  
CURRENT APPLICATION NUMBER: US/10/008,739A  
CURRENT FILING DATE: 2002-04-15  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 2  
LENGTH: 907  
TYPE: PRT  
ORGANISM: Canine  
US-10-008-739A-2

Query Match 98.4%; Score 1349.5; DB 14; Length 907;  
Best Local Similarity 99.6%; Pred. No. 6.9e-142;  
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 2 SHMIEGYECOPIFLNTVLEAIEPVGVCAGHDNNOPDSFALLSSINELGERRQLVHVMKAK 61  
Db 650 SH-IEGYECOPIFLNTVLEAIEPVGVCAGHDNNOPDSFALLSSINELGERRQLVHVMKAK 708  
QY 62 ALPFRNLHVDDQNAVIOYSWGLMVFAMGWRSPFTNVSRMLYFAPDLVFNERYMHSRM 121  
Db 709 ALPFRNLHVDDQNAVIOYSWGLMVFAMGWRSPFTNVSRMLYFAPDLVFNERYMHSRM 768  
QY 122 YSQCVRMRHLSQBFQWLTQTPQEFLLCMKALLFSIIPVGLKQKQFDELMNYIKELDR 181  
Db 769 YSQCVRMRHLSQBFQWLTQTPQEFLLCMKALLFSIIPVGLKQKQFDELMNYIKELDR 828  
QY 182 IIAKCKRNPFTSCSRFFQTLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMMARITIS 241  
Db 829 IIAKCKRNPFTSCSRFFQTLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMMARITIS 888  
QY 242 VQVFKILSGKVKPIYFHTQ 260  
Db 889 VQVFKILSGKVKPIYFHTQ 907

## RESULT 4

US-10-205-823-36  
Sequence 36, Application US/10205823  
Publication No. US20030108963A1  
GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John B.  
APPLICANT: Endege, Wilson O.  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Gorbacheva, Bella  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Kamelkar, Shubhangi  
APPLICANT: Monsey, Angela M.  
APPLICANT: Giac, Karen  
APPLICANT: Zhao, Xumei  
APPLICANT: Anderson, Dustin  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TREATMENT OF PROSTATE CANCER  
FILE REFERENCE: NRI-044  
CURRENT APPLICATION NUMBER: US/10/205,823  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307,982  
PRIOR FILING DATE: 2001-07-25  
PRIOR APPLICATION NUMBER: 60/314,356  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/325,020  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 60/341,746  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/362,158  
PRIOR FILING DATE: 2002-03-05  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 36  
LENGTH: 919  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-205-823-36

Query Match 98.4%; Score 1349.5; DB 15; Length 919;  
Best Local Similarity 99.6%; Pred. No. 7e-142;





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; SEQUENCE: 129
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-207-655-63
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; Query Match
; Best Local Similarity 55.8%; Score 765; DB 10; Length 314;
; Matches 137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;
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; 12 PIFNLVLEAIPGVGAGHNNQDPSPALLSLNLEGEROLVHVYVAKAKALPGFRNLAV 71
; 133 SOEFGWLOITPOEFLCMKALLFSIIPVDGLKNQKPEDELRMYIKELDRILACKRKNPT 191
; 130 PQEFLVQVSGERFLCMKRVLLNTIIPLEGRLSQOTQPEERMSSTYRELKALIGLRQGVV 189
;
; 192 SCRRRFQTLTKLDSVQPIARELHOFTEDLLIKSHMVSVDPEEMAAIISVQVKILSGK 251
; 190 SSSQRFQTLTKLNDLNDLHVQKQLHYCLNTFIQSRALSVPEPMMSVIAAQLPKILAGM 249
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; 252 VKPIYFH 258
; 250 VKPLLFH 256

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; SEQUENCE: 280
; Publication No. US20020197670A1
; GENERAL INFORMATION:
; APPLICANT: PRICE, THOMAS M.
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROGESTERONE RECEPTOR
; FILE REFERENCE: GHS-338
; CURRENT APPLICATION NUMBER: US/09/887,280
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/213,340
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-887-280-4
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; Query Match
; Best Local Similarity 55.8%; Score 765; DB 10; Length 314;
; Matches 137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;
;
; 12 PIFNLVLEAIPGVGAGHNNQDPSPALLSLNLEGEROLVHVYVAKAKALPGFRNLAV 71
; 66 PPLNLMSIEPDIYAGHNTKPTSSLLTSLNQLGERQLSVYKMSKSLPGFRNLHI 125
; 72 DDQNAVIOYSWGLMVFAMGRSFNTNNSRMLYFAPDLVENEYRMRKSRMYSOCVRMHL 131
; 126 DDQITLIQYSWMSLWVFGIGWRSYKGVSGQMLYFAPDLINLQERMSKSSFYSLCLTMWQI 185
;
; 132 SOEFGWLOITPOEFLCMKALLFSIIPVDGLKNQKPEDELRMYIKELDRILACKRKNPT 191
; 186 PQEFLVQVSGERFLCMKRVLLNTIIPLEGRLSQOTQPEERMSSTYRELKALIGLRQGVV 245
;
; 192 SCRRRFQTLTKLDSVQPIARELHOFTEDLLIKSHMVSVDPEEMAAIISVQVKILSGK 251
; 246 SSSQRFQTLTKLNDLNDLHVQKQLHYCLNTFIQSRALSVPEPMMSVIAAQLPKILAGM 305
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; 252 VKPIYFH 258
; 306 VKPLLFH 312

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-207-655-63

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; Query Match
; Best Local Similarity 55.8%; Score 765; DB 15; Length 933;
; Matches 137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;

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; 12 PIFNLVLEAIPGVGAGHNNQDPSPALLSLNLEGEROLVHVYVAKAKALPGFRNLAV 71
; 685 PPLNLMSIEPDIYAGHNTKPTSSLLTSLNQLGERQLSVYKMSKSLPGFRNLHI 744
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; 72 DDQNAVIOYSWGLMVFAMGRSFNTNNSRMLYFAPDLVENEYRMRKSRMYSOCVRMHL 131
; 745 DDQITLIQYSWMSLWVFGIGWRSYKGVSGQMLYFAPDLINLQERMSKSSFYSLCLTMWQI 804
;
; 132 SOEFGWLOITPOEFLCMKALLFSIIPVDGLKNQKPEDELRMYIKELDRILACKRKNPT 191
; 805 PQEFLVQVSGERFLCMKRVLLNTIIPLEGRLSQOTQPEERMSSTYRELKALIGLRQGVV 864
;
; 192 SCRRRFQTLTKLDSVQPIARELHOFTEDLLIKSHMVSVDPEEMAAIISVQVKILSGK 251
; 865 SSSQRFQTLTKLNDLNDLHVQKQLHYCLNTFIQSRALSVPEPMMSVIAAQLPKILAGM 924
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; 252 VKPIYFH 258
; 925 VKPLLFH 931

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; RESULT 10
; US-09-905-176-13
; Sequence 13, Application US/09905176
; Patent No. US20020150906A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: Debe, Derek A.
; TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM P
; FILE REFERENCE: 265/297
; CURRENT APPLICATION NUMBER: US/09/905,176
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/218,016
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-905-176-13

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; Query Match
; Best Local Similarity 53.1%; Score 728; DB 10; Length 240;
; Matches 131; Conservative 55; Mismatches 51; Indels 0; Gaps 0;

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; 12 PIFNLVLEAIPGVGAGHNNQDPSPALLSLNLEGEROLVHVYVAKAKALPGFRNLAV 71
; 4 PPLNLMSIEPDIYAGHNTKPTSSLLTSLNQLGERQLSVYKMSKSLPGFRNLHI 63
;
; 72 DDQNAVIOYSWGLMVFAMGRSFNTNNSRMLYFAPDLVENEYRMRKSRMYSOCVRMHL 131
; 64 DDQITLIQYSWMSLWVFGIGWRSYKGVSGQMLYFAPDLINLQERMSKSSFYSLCLTMWQI 123
;
; 132 SOEFGWLOITPOEFLCMKALLFSIIPVDGLKNQKPEDELRMYIKELDRILACKRKNPT 191
; 124 PQEFLVQVSGERFLCMKRVLLNTIIPLEGRLSQOTQPEERMSSTYRELKALIGLRQGVV 183
;
; 192 SCRRRFQTLTKLDSVQPIARELHOFTEDLLIKSHMVSVDPEEMAAIISVQVKIL 248
; 184 SSSQRFQTLTKLNDLNDLHVQKQLHYCLNTFIQSRALSVPEPMMSVIAAQLPKIL 240

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Db 613 QLTGWNASSORFHTKMDAMHEIVKXNLYCLSTFIOAEANOVPEPMSEVITSQ 672

QY 244 VKPIISGVKPIYFH 258

Db 673 LPKVLAVGVRPLLFH 687

## RESULT 14

US-10-001-486B-2

Sequence 2, Application US/10001486B

Publication No. US20030082642A1

## GENERAL INFORMATION:

APPLICANT: The Government of the United States of America

as represented by the Secretary

Department of Health and Human Services

Washington, D.C.

Hcun Ph.D., Han

Hager Ph.D., Gordon L.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MONITORING

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Needle & Rosenberg

STREET: 127 Peachtree Street, Suite 1200

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/001,486B

FILING DATE: 15-No. US20030082642A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/008,373

FILING DATE: 08 Dec 1995

ATTORNEY/AGENT INFORMATION:

NAME: Selby, Elizabeth

REGISTRATION NUMBER: 38298

REFERENCE/DOCKET NUMBER: 14014.0183

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-688-0770

TELEFAX: 404-688-9880

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1070 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-001-486B-2

Query Match

Best Local Similarity 46.6%; Score 639.5; DB 15; Length 1070;

Matches 122; Conservative 48; Mismatches 76; Indels 1; Gaps 1;

QY 12 PIFLVNLEAIEPGVYAGHNNOPDSFALLSLNEIGEROLVHVYKAKALPGFRNLHV 71

Db 823 PIVVLELVEIEPEVLYAGIDSSVPSAMRIMTILNMGQVIAAVKAKALIGLRNLHL 882

QY 72 DDQMAVIOYSWMGLVFMWGRSFTNVNSRMLYFAPDLVENEYRMHKSRYMSQCVRMRL 131

Db 883 DDQMTLLQYSWMFLWAFALGWRSGYSGNLLCFAPDLINQGRMSLPQMTDCKHMLFV 942

QY 132 SOEFGMLQITPOEFLCKKALLPSIIPVDGLNOKFPDELRLNRYIKELDRITACKRKPT 191

Db 943 SSELQRLQVSYEBYLCKMTLLLSVPEKGLKSQELFDEIRMTYIKELGKALVKEGNS 1002

QY 192 SCSRRFYQLTKLDSVQPIARELHOFITFDLLIKSHMVSVDPEPMMAEIIISVQPKILSGK 251

Db 1003 QNMGRFYQLTKLDSVQPIARELHOFITFDLLIKSHMVSVDPEPMMAEIIISVQPKILSGK 1061

QY 252 VKPIYFH 258

Db 1062 IKKLLFH 1068

## RESULT 15

US-09-853-450-20

Sequence 20, Application US/09853450

Publication No. US20020194645A1

## GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

APPLICANT: Pelaz, Soraya

APPLICANT: Ditta, Gary

TITLE OF INVENTION: The Regents of the University of California

TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants

FILE REFERENCE: 19452A-002400US

CURRENT APPLICATION NUMBER: US/09/853,450

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 20

LENGTH: 284

TYPE: PRT

ORGANISM: Rattus norvegicus

FEATURE:

OTHER INFORMATION: rat glucocorticoid receptor ligand binding domain

US-09-853-450-20

Query Match

Best Local Similarity 46.0%; Score 630.5; DB 10; Length 284;

Matches 121; Conservative 48; Mismatches 77; Indels 1; Gaps 1;

QY 12 PIFLVNLEAIEPGVYAGHNNOPDSFALLSLNEIGEROLVHVYKAKALPGFRNLHV 71

Db 37 PIVVLELVEIEPEVLYAGIDSSVPSAMRIMTILNMGQVIAAVKAKALIGLRNLHL 96

QY 72 DDQMAVIOYSWMGLVFMWGRSFTNVNSRMLYFAPDLVENEYRMHKSRYMSQCVRMRL 131

Db 97 DDQMTLLQYSWMFLWAFALGWRSGYSGNLLCFAPDLINQGRMSLPQMTDCKHMLFV 156

QY 132 SOEFGMLQITPOEFLCKKALLPSIIPVDGLNOKFPDELRLNRYIKELDRITACKRKPT 191

Db 157 SSELQRLQVSYEBYLCKMTLLLSVPEKGLKSQELFDEIRMTYIKELGKALVKEGNS 216

QY 192 SCSRRFYQLTKLDSVQPIARELHOFITFDLLIKSHMVSVDPEPMMAEIIISVQPKILSGK 251

Db 217 QNMGRFYQLTKLDSVQPIARELHOFITFDLLIKSHMVSVDPEPMMAEIIISVQPKILSGK 275

QY 252 VKPIYFH 258

Db 276 IKKLLFH 282

Search completed: October 9, 2003, 11:43:39

Job time : 28 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 9, 2003, 11:39:53 ; Search time 19 Seconds  
(Without alignments)

578.991 Million cell updates/sec

Title: US-09-687-609A-1  
Perfect score: 1371  
Sequence: 1 GSMIRGVEQPIFLNVLRA.....SVGVPRILSGKVKPIYFHQ 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/1aa/5A COMB .pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB .pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB .pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB .pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCUS COMB .pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349.5	98.4	452	3	US-08-764-870-16
2	1349.5	98.4	452	3	US-08-980-115-16
3	1349.5	98.4	918	3	US-09-041-886-11
4	765	55.9	363	6	5223606-6
5	765	55.8	933	3	US-08-764-870-14
6	765	55.8	933	3	US-08-980-115-14
7	665	48.5	984	3	US-08-764-870-15
8	665	48.5	984	3	US-08-980-115-15
9	662.5	48.3	777	3	US-08-764-870-13
10	662.5	48.3	777	3	US-08-980-115-13
11	644.5	47.0	534	3	US-08-875-223-8
12	639.5	46.6	1070	4	US-09-091-042A-2
13	638.5	46.6	284	2	US-08-592-214A-24
14	638.5	46.6	284	3	US-09-149-976-24
15	638.5	46.6	795	1	US-07-716-827C-5
16	630.5	46.0	284	3	US-08-659-188-20
17	630.5	46.0	284	3	US-08-655-227-20
18	630.5	46.0	284	3	US-08-655-241-20
19	630.5	46.0	284	4	US-09-398-326-20
20	626	45.7	356	6	5223606-7
21	224	16.3	60	5	PCT-US94-14074-1
22	211.5	15.4	596	2	US-08-836-620A-16
23	209	15.2	460	4	US-09-393-839-4
24	207.5	15.1	595	3	US-08-764-870-12
25	207.5	15.1	595	3	US-08-980-115-12
26	206.5	15.1	484	2	US-08-836-620A-13
27	206.5	15.1	485	2	US-08-836-620A-2

28	205	15.0	228	3	US-09-249-645-2	Sequence 2, Appl
29	205	15.0	228	4	US-09-844-132B-2	Sequence 2, Appl
30	204.5	14.9	591	2	US-08-836-620A-17	Sequence 17, Appl
31	204.5	14.9	595	3	US-09-041-886-35	Sequence 35, Appl
32	204.5	14.9	595	4	US-08-453-998-2	Sequence 2, Appl
33	204.5	14.9	651	3	US-08-693-940-3	Sequence 3, Appl
34	204.5	14.9	651	3	US-09-566-660-3	Sequence 3, Appl
35	204.5	14.9	773	3	US-08-564-264-1	Sequence 1, Appl
36	203.5	14.8	485	2	US-08-836-620A-3	Sequence 3, Appl
37	203.5	14.8	548	3	US-09-139-617-1	Sequence 1, Appl
38	203.5	14.8	548	4	US-09-561-741A-1	Sequence 1, Appl
39	203.5	14.8	548	4	US-09-558-795-1	Sequence 1, Appl
40	203	14.8	384	2	US-08-836-620A-15	Sequence 15, Appl
41	202.5	14.8	264	4	US-09-660-979-1	Sequence 1, Appl
42	200.5	14.6	229	3	US-09-249-645-1	Sequence 1, Appl
43	198.5	14.5	484	2	US-08-836-620A-14	Sequence 14, Appl
44	198.5	14.5	485	2	US-08-836-620A-5	Sequence 5, Appl
45	196.5	14.3	229	4	US-09-844-132B-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-764-870-16  
Sequence 16, Application US/08764870  
Patent No. 6236946  
GENERAL INFORMATION:  
APPLICANT: Scanlan, Thomas S  
APPLICANT: Baxter, John D  
APPLICANT: Pletterick, Robert J  
APPLICANT: Wagner, Richard L  
APPLICANT: Kushner, Peter J  
APPLICANT: Apriletti, James W  
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
TITLE OF INVENTION: Binding Domains  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Cooley Godward  
STREET: Five Palo Alto Square, 3000 El Camino Real  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,870  
CLASSIFICATION: 530  
FILING DATE: 13-DEC-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,540  
FILING DATE: 13-DEC-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,543  
FILING DATE: 13-DEC-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,606  
FILING DATE: 14-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Jackie N  
REGISTRATION NUMBER: 35, 966  
REFERENCE/DOCKET NUMBER: UCAL-246/01US  
TELECOMMUNICATION: (650) 843-5000  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TYPE: amino acid

STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-764-870-16

Query Match 98.4%; Score 1349.5; DB 3; Length 452;  
Best Local Similarity 99.6%; Pred. No. 9.1e-147;  
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSLNLSLGERQLVHVVMKAK 61  
DB 195 SH-IEGYECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSLNLSLGERQLVHVVMKAK 253  
QY 62 ALPGFNLHVDDQMAVIOYSWGLVFPAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 121  
DB 254 ALPGFNLHVDDQMAVIOYSWGLVFPAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 313  
QY 122 YSQCVRMRHLSOBFGLQITPOEFLCMKALLFSIIPVDGLKNOKFPDELIRNMYIKELDR 181  
DB 314 YSQCVRMRHLSOBFGLQITPOEFLCMKALLFSIIPVDGLKNOKFPDELIRNMYIKELDR 373  
QY 182 IIAKCRKNPTSCSRPFYQTLKLDVSQPIARELHQFTFDLLIKSHMVSVDPEPMMAEIIIS 241  
DB 374 IIAKCRKNPTSCSRPFYQTLKLDVSQPIARELHQFTFDLLIKSHMVSVDPEPMMAEIIIS 433  
QY 242 VQVPKILSGKVPYIFHTQ 260  
DB 434 VQVPKILSGKVPYIFHTQ 452

RESULT 2  
US-08-980-115-16  
; Sequence 16, Application US/08980115  
; Patent No. 6266622

GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S.  
; APPLICANT: Baxter, John D.  
; APPLICANT: Fletcher, Robert J.  
; APPLICANT: Wagner, Richard L.  
; APPLICANT: Kushner, Peter J.  
; APPLICANT: Apriletti, James W.  
; APPLICANT: West, Brian L.  
; APPLICANT: Shiau, Andrew K.  
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
; FILING DATE: 1997-11-26  
; CURRENT FILING DATE: 1997-11-26  
; EARLIER FILING DATE: 1996-12-13  
; EARLIER FILING DATE: 1996-12-13  
; EARLIER FILING DATE: 1995-12-14  
; EARLIER FILING DATE: 1995-12-14  
; EARLIER FILING DATE: 1995-12-13  
; EARLIER FILING DATE: 1995-12-13  
; EARLIER FILING DATE: 1995-12-13  
; EARLIER FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentm Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 452  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (184)..(437)  
; OTHER INFORMATION: minimal ligand binding domain  
US-08-980-115-16

Query Match 98.4%; Score 1349.5; DB 3; Length 452;  
Best Local Similarity 99.6%; Pred. No. 9.1e-147;  
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 2 SHMIEGECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSLNLSLGERQLVHVVMKAK 61

DB 195 SH-IEGYECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSLNLSLGERQLVHVVMKAK 253  
QY 62 ALPGFNLHVDDQMAVIOYSWGLVFPAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 121  
DB 254 ALPGFNLHVDDQMAVIOYSWGLVFPAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 313  
QY 122 YSQCVRMRHLSOBFGLQITPOEFLCMKALLFSIIPVDGLKNOKFPDELIRNMYIKELDR 181  
DB 314 YSQCVRMRHLSOBFGLQITPOEFLCMKALLFSIIPVDGLKNOKFPDELIRNMYIKELDR 373  
QY 182 IIAKCRKNPTSCSRPFYQTLKLDVSQPIARELHQFTFDLLIKSHMVSVDPEPMMAEIIIS 241  
DB 374 IIAKCRKNPTSCSRPFYQTLKLDVSQPIARELHQFTFDLLIKSHMVSVDPEPMMAEIIIS 433  
QY 242 VQVPKILSGKVPYIFHTQ 260  
DB 434 VQVPKILSGKVPYIFHTQ 452

RESULT 3  
US-09-041-886-11  
; Sequence 11, Application US/09041886  
; Patent No. 6235872

GENERAL INFORMATION:  
; APPLICANT: Bredesen, Dale B.  
; APPLICANT: Rabinzadeh, Sharoz  
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence  
; TITLE OF INVENTION: Polypeptides and Methods of Use  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentm Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/041,886  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2626  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 918 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-041-886-11

Query Match 98.4%; Score 1349.5; DB 3; Length 918;  
Best Local Similarity 99.6%; Pred. No. 2.6e-146;  
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSLNLSLGERQLVHVVMKAK 61  
DB 661 SH-IEGYECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSLNLSLGERQLVHVVMKAK 719  
QY 62 ALPGFNLHVDDQMAVIOYSWGLVFPAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 121  
DB 720 ALPGFNLHVDDQMAVIOYSWGLVFPAMGWSFTNVNSRMLYFAPDLVFNERYRHKSRM 779  
QY 122 YSQCVRMRHLSOBFGLQITPOEFLCMKALLFSIIPVDGLKNOKFPDELIRNMYIKELDR 181

Db 780 YSQCVRHSHSQEFGWLTQTPQEFCKMALLFSIIPVDGLKNOKFPDELMNYIKELDR 839  
 Qy 182 IICCKRNPTSCSRFPQTLKLDVQPIARELHOFTDILIKSHNVSDPPEMAIIS 241  
 Db 840 IICCKRNPTSCSRFPQTLKLDVQPIARELHOFTDILIKSHNVSDPPEMAIIS 899  
 Qy 242 VOVPKILSGKVPYIFFTQ 260  
 Db 900 VOVPKILSGKVPYIFFTQ 918

## RESULT 4

5223606-6  
 Patent No. 5223606  
 APPLICANT: BLADIN DE THE, HUGHES, MARCHIO, AGNES, TIOLLAIS,  
 PIERRE, DEJEAN, ANNE  
 TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED  
 PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA  
 NUMBER OF SEQUENCES: 11  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/134,130  
 FILING DATE: 17-DEC-1987  
 PRIOR APPLICATION DATA:  
 SEQ ID NO: 6:  
 LENGTH: 363  
 5223606-6

Query Match 55.9%; Score 766; DB 6; Length 363;  
 Best Local Similarity 55.5%; Pred. No. 1,1e-79;  
 Matches 137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;

Qy 12 PIFLVNLAIEIPGVGAGHNNOPDSFALLSINELGROLVHVYKAKALPGFNNLHV 71  
 Db 115 PPLINLMSIEPDVIAIGHDNTPKPTSSSLTSLINQIGROLVSVKMSKLPGRNLIH 174  
 Qy 72 DDQMAVIOYSGMGLVFWGMSFTNNVSRMLYFAPDLVFNEMHKSRYMSQCVRRHL 131  
 Db 175 DDQITLQYSGMGLVFWGMSFTNNVSRMLYFAPDLVFNEMHKSRYMSQCVRRHL 234  
 Qy 132 SOEFGWLQTPQEFCKMALLFSIIPVDGLKNOKFPDELMNYIKELDR IICCKRNPT 191  
 Db 235 POEFGWLQTPQEFCKMALLFSIIPVDGLKNOKFPDELMNYIKELDR IICCKRNPT 294  
 Qy 192 SCGRFPQTLKLDVQPIARELHOFTDILIKSHNVSDPPEMAIISVOVPKILSGK 251  
 Db 295 SSSQRFYQTLKLDVQPIARELHOFTDILIKSHNVSDPPEMAIISVOVPKILSGK 354  
 Qy 252 VKPIYFH 258  
 Db 355 VKPLLFH 361

## RESULT 5

US-08-764-870-14  
 Sequence 14, Application US/08764870  
 Patent No. 6236946  
 GENERAL INFORMATION:  
 APPLICANT: Scanlan, Thomas S  
 APPLICANT: Baxter, John D  
 APPLICANT: Fleeterick, Robert J  
 APPLICANT: Wagner, Richard L  
 APPLICANT: Kushner, Peter J  
 APPLICANT: Apiletti, James W  
 TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
 TITLE OF INVENTION: Binding Domains  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooley Godward  
 STREET: Five Palo Alto Square, 3000 El Camino Real  
 CITY: Palo Alto  
 STATE: CA

COUNTRY: USA  
 ZIP: 94306  
 COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/764,870  
 FILING DATE: 13-DEC-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/008,540  
 FILING DATE: 13-DEC-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/008,543  
 FILING DATE: 13-DEC-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/008,606  
 FILING DATE: 14-DEC-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Nakamura, Jackie N

REGISTRATION NUMBER: 35,966  
 REFERENCE/DOCKET NUMBER: UCAL-246/01US

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650)843-5000

INFORMATION FOR SEQ. ID NO. 14:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 933 amino acids

TYPE: amino acid  
 STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-764-870-14  
 Query Match 55.8%; Score 765; DB 3; Length 933;  
 Best Local Similarity 55.5%; Pred. No. 5,6e-79;  
 Matches 137; Conservative 57; Mismatches 53; Indels 0; Gaps 0;

Qy 12 PIFLVNLAIEIPGVGAGHNNOPDSFALLSINELGROLVHVYKAKALPGFNNLHV 71  
 Db 685 PPLINLMSIEPDVIAIGHDNTPKPTSSSLTSLINQIGROLVSVKMSKLPGRNLIH 744  
 Qy 72 DDQMAVIOYSGMGLVFWGMSFTNNVSRMLYFAPDLVFNEMHKSRYMSQCVRRHL 131  
 Db 745 DDQITLQYSGMGLVFWGMSFTNNVSRMLYFAPDLVFNEMHKSRYMSQCVRRHL 804  
 Qy 132 SOEFGWLQTPQEFCKMALLFSIIPVDGLKNOKFPDELMNYIKELDR IICCKRNPT 191  
 Db 805 POEFGWLQTPQEFCKMALLFSIIPVDGLKNOKFPDELMNYIKELDR IICCKRNPT 864  
 Qy 192 SCGRFPQTLKLDVQPIARELHOFTDILIKSHNVSDPPEMAIISVOVPKILSGK 251  
 Db 865 SSSQRFYQTLKLDVQPIARELHOFTDILIKSHNVSDPPEMAIISVOVPKILSGK 924  
 Qy 252 VKPIYFH 258  
 Db 925 VKPLLFH 931

## RESULT 6

US-08-980-115-14  
 Sequence 14, Application US/08980115  
 Patent No. 626622  
 GENERAL INFORMATION:  
 APPLICANT: Scanlan, Thomas S  
 APPLICANT: Baxter, John D  
 APPLICANT: Fleeterick, Robert J  
 APPLICANT: Wagner, Richard L  
 APPLICANT: Kushner, Peter J  
 APPLICANT: Apiletti, James W  
 APPLICANT: West, Brian L  
 APPLICANT: Shlau, Andrew K.





EARLIER APPLICATION NUMBER: 08/764,870  
EARLIER FILING DATE: 1996-12-13  
EARLIER APPLICATION NUMBER: 60/008,606  
EARLIER FILING DATE: 1995-12-14  
EARLIER APPLICATION NUMBER: 60/008,543  
EARLIER FILING DATE: 1995-12-13  
EARLIER APPLICATION NUMBER: 60/008,540  
EARLIER FILING DATE: 1995-12-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 15  
LENGTH: 984  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (695)..(969)  
OTHER INFORMATION: minimal ligand binding domain  
US-08-980-115-15

Query Match 48.5%; Score 665; DB 3; Length 984;  
Best Local Similarity 52.9%; Pred. No. 2e-67; Indels 0; Gaps 0;  
Matches 128; Conservative 44; Mismatches 70;

QY 17 VLEAIEPGVAGHNNQDPSFALLSLNIEGROLVHVYKAKALPGRNLAHYDDQMA 76  
DB 741 VLENIEPRVYGVGYSSKEDTAMENLSTNRLAGKQMTQVYKAYLPGFKLPLEDQIT 800  
QY 77 VIQVSMGLVAMGMRSEFTVNSRMLYPAPDLVNEVYKMRYSQCVRMHLISOFG 136  
DB 801 LIQVSMGLSFPALSMRSYKHTNSQFLVYAPDLVNEVYKMRYSQCVRMHLISOFG 860  
QY 137 WLOIIPORFLCKALLPSIIPVDGLKNOKPFDELRMYTKELDRILACKRNPISCSRR 196  
DB 861 RLQLFEEYTTINKVLLSTIPKDKLSQAAPEERNTYIKELRQVTKCPNNSQSQMOR 920  
QY 197 FYQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEEMAEIISVOVKILSGKKEFY 256  
DB 921 FYQLTKLDSMDVLDLIFPCYTPRBSHAKVFPMLVYIIDLQPKVSGNAKELY 980  
QY 257 FH 258  
DB 981 FH 982

RESULT 9  
US-08-764-870-13  
Sequence 13, Application US/08764870  
Patent No. 6236946  
GENERAL INFORMATION:

APPLICANT: Scanlan, Thomas S  
APPLICANT: Baxter, John D  
APPLICANT: Pletterick, Robert J  
APPLICANT: Wagner, Richard L  
APPLICANT: Kushner, Peter J  
APPLICANT: Apriletti, James W  
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Godward  
STREET: Five Palo Alto Square, 3000 El Camino Real  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,870  
FILING DATE: 13-DEC-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,540  
FILING DATE: 13-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,543  
FILING DATE: 13-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,606  
FILING DATE: 14-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Jackie N  
REGISTRATION NUMBER: 35,966  
REFERENCE/DOCKET NUMBER: UCAL-246/01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 843-5000  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 777 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-764-870-13

Query Match 48.3%; Score 662.5; DB 3; Length 777;  
Best Local Similarity 50.6%; Pred. No. 2.7e-67;  
Matches 125; Conservative 49; Mismatches 72; Indels 1; Gaps 1;

QY 12 PIPNLVLAIEPGVAGHNNQDPSFALLSLNIEGROLVHVYKAKALPGRNLAHY 71  
DB 530 PTLVSLVLEPELVYGVYSSVSDSTWRTMTTNLNGROVIAVYKAKALPGRNLAHY 589  
QY 72 DDQMAVIOVSMGLVAMGMRSEFTVNSRMLYPAPDLVNEVYKMRYSQCVRMHL 131  
DB 590 DDQMTLLQVSMGLVAMGMRSEFTVNSRMLYPAPDLVNEVYKMRYSQCVRMHL 649  
QY 132 SQEFGMLQITPQFLCKALLPSIIPVDGLKNOKPFDELRMYTKELDRILACKRNP 191  
DB 650 SSEIHLRLQVSEYETLCKMTLLLSVPEKDKLSQELDEIRMTYIKELGKAIYREGNSS 709  
QY 192 SCRRFYQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEEMAEIISVOVKILSG 251  
DB 710 QNWRFYQLTKLDSMDVLDLIFPCYTPRBSHAKVFPMLVYIIDLQPKVSGNAKELY 768  
QY 252 VKPIYFH 258  
DB 769 IKLLIFH 775

RESULT 10  
US-08-980-115-13  
Sequence 13, Application US/08980115  
Patent No. 6266622  
GENERAL INFORMATION:

APPLICANT: Scanlan, Thomas S.  
APPLICANT: Baxter, John D.  
APPLICANT: Pletterick, Robert J.  
APPLICANT: Wagner, Richard L.  
APPLICANT: Kushner, Peter J.  
APPLICANT: Apriletti, James W.  
APPLICANT: Shiue, Brian L.  
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS  
FILE REFERENCE: UCAL-246/01US  
CURRENT APPLICATION NUMBER: US/08/980,115  
FILING DATE: 1997-11-26  
EARLIER APPLICATION NUMBER: 08/764,870  
EARLIER FILING DATE: 1996-12-13  
EARLIER APPLICATION NUMBER: 60/008,606  
EARLIER FILING DATE: 1995-12-14

EARLIER APPLICATION NUMBER: 60/008,543  
 EARLIER FILING DATE: 1995-12-13  
 EARLIER APPLICATION NUMBER: 60/008,540  
 EARLIER FILING DATE: 1995-12-13  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 13  
 LENGTH: 777  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (506)..(762)  
 OTHER INFORMATION: minimal ligand binding domain  
 US-08-980-115-13

Query Match 48.3%; Score 662.5; DB 3; Length 777;  
 Best Local Similarity 50.6%; Pred. No. 2.7e-67;  
 Matches 125; Conservative 49; Mismatches 72; Indels 1; Gaps 1;

QY 12 PFLNVLAIIPGVCAHDNDNDPDSFALLSSINELIGEROLVHVYKMAKALPGFRLHIV 71  
 DB 530 PTLVSLLEYEPVLYAGYDSSVPSDSTWRIMTLNMLGGRQVLAAYKMAKALPGFRLHIV 589  
 QY 72 DDGMVIOYSWGLMTPFAMGMSFTVNSMLYFADLVFNERYMKSRMYSOCVAMRL 131  
 DB 590 DDGMTLLQYSWMLFAPALGMSRYROSSANLCPADPLINEGRMTLPCHYDCKMLYV 649  
 QY 132 SOEFGMLQITPOBFLCMKALLPSIIPVDGLKNQKFEDELNMVYKELDRILACKRKNPT 191  
 DB 650 SEELHLOYSYERHLCMKTLILLSSVFKDLSQBELFDEIRMTYIKELGKALYKREGNS 709  
 QY 192 SCGRFFYQTLKLDSDVQPIARELHQFTDLLIKSHVSDVPEPMARIIISVQPKILSGK 251  
 DB 710 QMWRFYQTLKLDSDHEVENLNYCFQTFDLKTM-SIEFPEMLARIITNOIPKYSNGN 768  
 QY 252 VKPIYFH 258  
 DB 769 IKKLPH 775

## RESULT 11

US-08-875-223-8

Sequence 8, Application US/08875223  
 Patent No. 6127175  
 GENERAL INFORMATION:  
 APPLICANT: VIGNE, Emmanuelle  
 APPLICANT: PERRICAUDET, Michel  
 APPLICANT: DEDIEU, Jean-Francois  
 APPLICANT: ORSINI, Cecile  
 APPLICANT: YEH, Patrice  
 APPLICANT: LATTA, Martine  
 APPLICANT: PROST, Edouard  
 TITLE OF INVENTION: CELLS FOR THE PRODUCTION OF RECOMBINANT  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 STREET: 500 Arcola Road, Mailstop 3C43  
 CITY: Colleagueville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/875,223  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/00747  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/06532  
 FILING DATE: 01-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 95/10541  
 FILING DATE: 08-SEP-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR WO FR96/00088  
 FILING DATE: 19-JAN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rehner Esq., Paul F.  
 REGISTRATION NUMBER: 35,135  
 REFERENCE/DOCKET NUMBER: ST9500561-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610) 454-3839  
 TELEFAX: (610) 454-3808  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 534 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-875-223-8

Query Match 47.0%; Score 644.5; DB 3; Length 534;  
 Best Local Similarity 51.3%; Pred. No. 1.8e-65;  
 Matches 122; Conservative 46; Mismatches 69; Indels 1; Gaps 1;

QY 21 IEPGVCAHDNDNDPDSFALLSSINELIGEROLVHVYKMAKALPGFRLHIVDDGMVIOY 80  
 DB 3 IEPVLVAGYDSSVPSDSTWRIMTLNMLGGRQVLAAYKMAKALPGFRLHIVDDMTLLQY 62  
 QY 81 SMGLMTPFAMGMSFTVNSMLYFADLVFNERYMKSRMYSOCVAMRLHISOEFGMLQI 140  
 DB 63 SMFLMPLGMSRYROSSANLCPADPLINEGRMTLPCHYDCKMLYVSSLEHLOV 122  
 QY 141 TPOBFLCMKALLPSIIPVDGLKNQKFEDELNMVYKELDRILACKRKNPTSCGRFFYQ 200  
 DB 123 SYEYLCKMTLLILLSSVFKDLSQBELFDEIRMTYIKELGKALYKREGNSQNMRFYQ 182  
 QY 201 TKLDSDVQPIARELHQFTDLLIKSHVSDVPEPMARIIISVQPKILSGVXPIYFH 258  
 DB 183 TKLDSDHEVENLNYCFQTFDLKTM-SIEFPEMLARIITNOIPKYSNGNKKILFH 239

## RESULT 12

US-09-091-042A-2

Sequence 2, Application US/09091042A  
 Patent No. 6455300  
 GENERAL INFORMATION:  
 APPLICANT: The Government of the United States of America  
 as represented by the Secretary  
 Department of Health and Human Services  
 Washington, D.C.  
 Hsuan Ph.D., Han  
 Hager Ph.D., Gordon L.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MONITORING  
 DNA BINDING MOLECULES IN LIVING CELLS  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Needle & Rosenberg  
 STREET: 127 Peachtree Street, Suite 1200  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/091.042A  
 FILING DATE: 08-Jun-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/008,373  
 FILING DATE: 08 Dec 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Selby, Elizabeth  
 REGISTRATION NUMBER: 38298  
 REFERENCE/DOCKET NUMBER: 14014.0183  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 404-688-0770  
 TELEFAX: 404-688-9880  
 INFORMATION FOR SEQ ID NO: 2:  
 LENGTH: 1070 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULAR TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-091-042A-2

Query Match 46.6%; Score 639.5; DB 4; Length 1070;  
 Best Local Similarity 49.4%; Pred. No. 2e-64;  
 Matches 122; Conservative 48; Mismatches 76; Indels 1; Gaps 1;  
 QY 12 PIFLVAVLEIIEBPGVVCAGHNNQPDSPALLSSINELGROLVHYVYKAKALPGFNNH 71  
 DB 823 PTVLSLEVIIEBPGVVCAGHNNQPDSPALLSSINELGROLVHYVYKAKALPGFNNH 882  
 QY 72 DDQMAVIOYSWMGLMVFAMGMSFTNVNSRMLYFAPDLVFNERYMKHSRMYSOCVRRH 131  
 DB 883 DDQMTLLQYSWMFLMVFAMGMSFTNVNSRMLYFAPDLVFNERYMKHSRMYSOCVRRH 942  
 QY 132 SQEFGMLQITPQFPLCMKALLFSIIPVDGLKNQKFPDELKNNYIKELDRIIACKRKNT 191  
 DB 943 SSELQRLQVSYREYLCKMTLLLSVPRGKLSQGLFDEIRMTYIKELGKALVKBGNS 1002  
 QY 192 SCSRRFYOLTKLDSVQPIARELHOFTDLIKSHMVSVDPEMAEIIISVQPKILSGK 251  
 DB 1003 QNMQRFYOLTKLDSMHEVEVNTLYCFOTFLDKTM-SIEFPMALAIITNQIPKYSNGN 1061  
 QY 252 VKRIYFH 258  
 DB 1062 IKKLIFH 1068

RESULT 13  
 US-08-592-214A-24  
 Sequence 24, Application US/08592214A  
 Patent No. 5811536  
 GENERAL INFORMATION:  
 APPLICANT: Yanofsky, Martin F.  
 TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
 TITLE OF INVENTION: Genes and Methods of Using Same  
 NUMBER OF SEQUENCES: 33  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/592,214A  
 FILING DATE: 26-JAN-1996

CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-UD 1927  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 284 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULAR TYPE: protein  
 US-08-592-214A-24

Query Match 46.6%; Score 638.5; DB 2; Length 284;  
 Best Local Similarity 49.4%; Pred. No. 3.5e-65;  
 Matches 122; Conservative 48; Mismatches 76; Indels 1; Gaps 1;  
 QY 12 PIFLVAVLEIIEBPGVVCAGHNNQPDSPALLSSINELGROLVHYVYKAKALPGFNNH 71  
 DB 37 PTVLSLEVIIEBPGVVCAGHNNQPDSPALLSSINELGROLVHYVYKAKALPGFNNH 96  
 QY 72 DDQMAVIOYSWMGLMVFAMGMSFTNVNSRMLYFAPDLVFNERYMKHSRMYSOCVRRH 131  
 DB 97 DDQMTLLQYSWMFLMVFAMGMSFTNVNSRMLYFAPDLVFNERYMKHSRMYSOCVRRH 156  
 QY 132 SQEFGMLQITPQFPLCMKALLFSIIPVDGLKNQKFPDELKNNYIKELDRIIACKRKNT 191  
 DB 157 SSELQRLQVSYREYLCKMTLLLSVPRGKLSQGLFDEIRMTYIKELGKALVKBGNS 216  
 QY 192 SCSRRFYOLTKLDSVQPIARELHOFTDLIKSHMVSVDPEMAEIIISVQPKILSGK 251  
 DB 217 QNMQRFYOLTKLDSMHEVEVNTLYCFOTFLDKTM-SIEFPMALAIITNQIPKYSNGN 275  
 QY 252 VKRIYFH 258  
 DB 276 IKKLIFH 282

RESULT 14  
 US-09-149-976-24  
 Sequence 24, Application US/09149976  
 Patent No. 6127123  
 GENERAL INFORMATION:  
 APPLICANT: Yanofsky, Martin F.  
 TITLE OF INVENTION: Cauliflower Floral Meristem Identity  
 TITLE OF INVENTION: Genes and Methods of Using Same  
 NUMBER OF SEQUENCES: 33  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Campbell & Flores LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/149,976  
 FILING DATE: 09-SEP-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/592,214  
 FILING DATE: 26-JAN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-UD 3291

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 284 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-149-976-24

Query Match 46.6%; Score 638.5; DB 3; Length 284;  
Best Local Similarity 49.4%; Pred. No. 3.5e-65;  
Matches 122; Conservative 48; Mismatches 76; Indels 1; Gaps 1;

QY 12 PFLNVLAIIEPGVCAHDNNOPDSFALLSSINELGSRQLVHVVKAKALPGFRNLHV 71  
DB 37 PTLVSLIEVIEPEVLVAGYDSSVPDSAMRLMTLNLGGRQVIAAVKAKALIGLRNLHL 96  
QY 72 DDQMAVIOYSWGLMVFAMGMSFTVNSRMLYFADPLVNEVYRHKSMYSOCYRMLTV 131  
DB 97 DDQMTLLQYSWGLMVFAMGMSFTVNSRMLYFADPLVNEVYRHKSMYSOCYRMLTV 156  
QY 132 SOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFPEDELMNYIKELDRITACKRKNPT 191  
DB 157 SSELQRLQVSYEYLCKMTLLLSVPRKGLSKQELFDEIRMTYIKELGKALVKBGNS 216  
QY 192 SCSRRFYQLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMAAIIISVQPKILSGK 251  
DB 217 QNWQRFYQLTKLDSMHEVENLITVCFQTFPLDKTM-SIEPPEMLAEIITNQIPKYSNGN 275  
QY 252 VKPIYFH 258  
DB 276 IKQLLFH 282

RESULT 15

US-07-716-827C-5

Sequence 5, Application US/07716827C  
Patent No. 5215916

GENERAL INFORMATION:

APPLICANT: Simone Jr., Stoney S.

APPLICANT: Yamamoto, K. R.

APPLICANT: Chakraborti, P. K.

APPLICANT: Garabedian, M. J.

TITLE OF INVENTION: SUPER GLUCOCORTICOID RECEPTORS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSER: Cushman, Darby &amp; Cushman

STREET: Elevench floor, 1615 L Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20036-5601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/716,827C

FILING DATE: 19910619

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Scott, Watson T.

REGISTRATION NUMBER: 26,581

REFERENCE/DOCKET NUMBER: WTS/5683/84453

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)8613000

TELEFAX: (202)822-8944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 795 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-716-827C-5

Query Match 46.6%; Score 638.5; DB 1; Length 795;  
Best Local Similarity 49.4%; Pred. No. 1.6e-64;  
Matches 122; Conservative 48; Mismatches 76; Indels 1; Gaps 1;

QY 12 PFLNVLAIIEPGVCAHDNNOPDSFALLSSINELGSRQLVHVVKAKALPGFRNLHV 71  
DB 548 PTLVSLIEVIEPEVLVAGYDSSVPDSAMRLMTLNLGGRQVIAAVKAKALIGLRNLHL 607  
QY 72 DDQMAVIOYSWGLMVFAMGMSFTVNSRMLYFADPLVNEVYRHKSMYSOCYRMLTV 131  
DB 608 DDQMTLLQYSWGLMVFAMGMSFTVNSRMLYFADPLVNEVYRHKSMYSOCYRMLTV 667  
QY 132 SOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFPEDELMNYIKELDRITACKRKNPT 191  
DB 668 SSELQRLQVSYEYLCKMTLLLSVPRKGLSKQELFDEIRMTYIKELGKALVKBGNS 727  
QY 192 SCSRRFYQLTKLDSVQPIARELHOFTFDLLIKSHMVSVDPEMAAIIISVQPKILSGK 251  
DB 728 QNWQRFYQLTKLDSMHEVENLITVCFQTFPLDKTM-SIEPPEMLAEIITNQIPKYSNGN 786  
QY 252 VKPIYFH 258  
DB 787 IKQLLFH 793

Search completed: October 9, 2003, 11:42:40  
Job time : 20 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 11:38:28 ; Search time 45 Seconds  
(without alignments)  
917.087 Million cell updates/sec

Title: US-09-687-609a-1  
Sequence: 1 GSHMIGYRCQPIFLNVLEA.....SVQPKILSGKXKPIYFHQ 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
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5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
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8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
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12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1371	100.0	260	22	AA97073
2	1349.5	98.4	388	20	AB883821
3	1349.5	98.4	452	20	AAV21627
4	1349.5	98.4	839	23	ABG71292
5	1349.5	98.4	839	23	AA668238
6	1349.5	98.4	895	24	AAE32995
7	1349.5	98.4	895	24	AAE32996
8	1349.5	98.4	899	24	AAE32589
9	1349.5	98.4	902	10	AA93110

10	1349.5	98.4	902	10	AA931006
11	1349.5	98.4	907	24	ABG74229
12	1349.5	98.4	918	20	AAV34991
13	1349.5	98.4	919	10	AA93096
14	1349.5	98.4	919	18	AAW14783
15	1349.5	98.4	919	21	AAV78914
16	1349.5	98.4	919	23	ABJ05582
17	1349.5	98.4	919	23	AAE19061
18	1349.5	98.4	919	24	ABJ19809
19	1346.5	98.2	918	12	AAE12223
20	1341.5	97.8	919	10	AA93109
21	1338.5	97.6	902	12	AAE12224
22	1326	96.7	252	24	ABU08036
23	1243	90.7	246	23	AAU75930
24	1179	86.0	250	22	AA65959
25	937	68.3	630	12	AAE12230
26	813.5	59.3	294	23	AB883822
27	765	55.8	251	21	AAE26786
28	765	55.8	251	23	ABJ15107
29	765	55.8	252	24	ABU08035
30	765	55.8	255	22	AAE97074
31	765	55.8	314	24	ABP70513
32	765	55.8	933	20	AAV21621
33	765	55.8	933	21	AAV7297
34	728	53.1	240	23	AAE17863
35	706	51.5	630	23	AB880765
36	706	51.5	630	23	AB880766
37	706	51.5	630	24	AAE35246
38	706	51.5	630	24	AAE35248
39	706	51.5	654	23	AB880764
40	706	51.5	654	24	AAE35245
41	702	51.2	448	24	AAE35247
42	666.5	48.6	483	24	ABP58319
43	666	48.6	215	23	AAE17861
44	665.5	48.5	257	24	ABU08045
45	665.5	48.5	777	24	ABU08024

## ALIGNMENTS

RESULT 1  
ID AAB97073 standard; Protein, 260 AA.

XX AAB97073;  
DT 31-JUL-2001 (first entry)

XX Rat androgen receptor ligand binding domain.

XX Rat; androgen receptor; AR; ligand binding domain; LBD; osteopathic;  
XX crystallographic structure; AR-LBD; AR modulator; prostate cancer;  
XX age related disease; osteoporosis; muscle wasting; libido; vasotropic;  
XX protein coordinate data.

OS Rattus sp.

XX WO200127622-A1.

XX 19-APR-2001.

XX 13-OCT-2000; 2000WO-US28495.

XX 14-OCT-1999; 99US-0159394.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Weinmann R, Einspahr HM, Krystek SR, Sack JS, Salvati ME;  
XX Tokarek JS, Wang C, Altar RM;

XX WPI; 2001-300222/31.

Rat androgen recep  
Canine Androgen re  
Human androgen rec  
Human androgen rec  
Androgen receptor.  
Human androgen rec  
Breast cancer-asso  
Human androgen rec  
Androgen-independe  
Human androgen rec  
Human androgen rec  
Rat androgen recep  
Human steroid rece  
Androgen receptor  
Human androgen rec  
Type/androgen rece  
Human androgen rec  
Human progesterone  
LBDG1 related prot  
Human steroid rece  
Rat progesterone r  
Andro acid sequenc  
Ligand binding dom  
Human progesterone  
Chain A of structu  
Geneswitch regulat  
Truncated GAL4 DBD  
PSI163 V.4.0 plas  
Geneswitch regulat  
pGLV65 plasmid ge  
Geneswitch regulat  
Glucocorticoid rec  
Chain A of structu  
Mutant human gluco  
Mutant human gluco

PT New crystallographic structure of the Androgen receptor ligand binding domain, useful for identifying modulators of androgen receptors -  
 PS Example; Page 27; 83pp; English.

CC The present sequence is the rat androgen receptor (AR) ligand-binding domain (LBD). It is provided in an example illustrating an invention relating to a new crystallographic structure of the AR-LBD. The structure comprises either an AR-LBD and an AR-LBD ligand, or an AR-LBD without an AR-LBD ligand (where the crystal diffracts to at least 3 angstrom resolution and has a crystal stability within 5 % of its unit cell dimensions). The AR-LBD is useful for identifying modulators of the androgen receptor, which may be used for treating prostate cancer and age related diseases such as osteoporosis, muscle wasting and loss of libido.

CC Sequence 260 AA;

Query Match 100.0%; Score 1371; DB 22; Length 260;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-135;  
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 GSHMIEGECOPFLNVLBAIEGVVCAHDNNDPSFALLSLNLSLGEROLVHVVKMA 60  
 1 GSHMIEGECOPFLNVLBAIEGVVCAHDNNDPSFALLSLNLSLGEROLVHVVKMA 60

QY 61 KALPGRNLAVDDOMAVIQYSWGLVFWFAMGWSFTNVNSRMLYFADLVFNERYMHKSR 120  
 DB 61 KALPGRNLAVDDOMAVIQYSWGLVFWFAMGWSFTNVNSRMLYFADLVFNERYMHKSR 120

QY 121 MSQCVRMRHLSQEPGLQITPQFLCMKALLFSIIPVDGLKNOKFPELNNYIKELD 180  
 DB 121 MSQCVRMRHLSQEPGLQITPQFLCMKALLFSIIPVDGLKNOKFPELNNYIKELD 180

QY 181 RIACRKNPTSCSRRYQTTLKLDVQPIARELHQTTPDLLKSHNVSVDPEMMAEIT 240  
 DB 181 RIACRKNPTSCSRRYQTTLKLDVQPIARELHQTTPDLLKSHNVSVDPEMMAEIT 240

QY 241 SVQPKILSGKVPRIYFHTQ 260  
 DB 241 SVQPKILSGKVPRIYFHTQ 260

RESULT 2  
 ABB83821 ID ABB83821 standard; Protein; 388 AA.

AC ABB83821;  
 XX  
 DT 13-SEP-2002 (first entry)

DE Human androgen receptor variant AR42 SRQ ID NO 2.  
 XX  
 KM Human; androgen receptor; receptor; AR; AR42; AR32; tumour; cancer;  
 KM steroid response element; prostate cancer; testis; gene therapy;  
 KM hormone therapy; cytostatic; contraceptive.

OS Homo sapiens.  
 XX  
 PN BP1213300-A1.  
 XX  
 PD 12-JUN-2002.  
 XX  
 PF 26-OCT-2001; 2001EP-0250379.  
 XX  
 PR 30-NOV-2000; 2000DB-1061161.  
 XX  
 PA (SCHD) SCHERING AG.  
 XX  
 PI Ahrens-Fath I, Haendler B,  
 XX  
 DR WPI; 2002-530575/57.  
 DR N-PSDB; ABN85656.

XX New nucleic acid encoding variant forms of androgen receptor; useful  
 PT for diagnosis and treatment of prostatic cancer; also related proteins  
 PS and antibodies -  
 XX  
 PS Claim 5; Page 9-11; 25pp; German.

CC The invention relates to a nucleic acid (I) that encodes an androgen receptor (AR) variant AR42 (ABN85656) or AR32 (ABN85657) or its equivalents or a sequence that hybridises to them under stringent conditions. Polypeptides (II, ABN83821-ABN83822) expressed by (I), can bind androgens and other ligands and form heterodimers which can bind to steroid response elements in target genes but do not induce activation, so act as repressors of the known AR. (II) are used to raise specific antibodies. (I) are used for recombinant production of (II) and as probes for detecting (I)-related nucleic acid in tumour tissue. Also (I), (II), CC a specific peptide and cells transfected with (I)-containing vectors, are useful for identifying effectors of (II), specifically antiandrogenic agents potentially useful for treating androgen-related diseases, e.g. cancer of prostate or testis and as male contraceptives. (I) can be used CC similarly in gene therapy. Antibodies to (II) are used to detect or CC quantify (II) in tumour tissue, e.g. to determine if resistance to hormone therapy is the result of altered expression of (II).

CC Sequence 388 AA;

Query Match 98.4%; Score 1349.5; DB 23; Length 388;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-132;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIEGECOPFLNVLBAIEGVVCAHDNNDPSFALLSLNLSLGEROLVHVVKMA 61  
 DB 131 SH-IEGYECOPFLNVLBAIEGVVCAHDNNDPSFALLSLNLSLGEROLVHVVKMA 189

QY 62 ALPGRNLAVDDOMAVIQYSWGLVFWFAMGWSFTNVNSRMLYFADLVFNERYMHKSR 121  
 DB 190 ALPGRNLAVDDOMAVIQYSWGLVFWFAMGWSFTNVNSRMLYFADLVFNERYMHKSR 249

QY 122 YQCVRMRHLSQEPGLQITPQFLCMKALLFSIIPVDGLKNOKFPELNNYIKELD 181  
 DB 250 YQCVRMRHLSQEPGLQITPQFLCMKALLFSIIPVDGLKNOKFPELNNYIKELD 309

QY 182 RIACRKNPTSCSRRYQTTLKLDVQPIARELHQTTPDLLKSHNVSVDPEMMAEIT 241  
 DB 310 RIACRKNPTSCSRRYQTTLKLDVQPIARELHQTTPDLLKSHNVSVDPEMMAEIT 369

QY 242 VQPKILSGKVPRIYFHTQ 260  
 DB 370 VQPKILSGKVPRIYFHTQ 388

RESULT 3  
 AAY21627 ID AAY21627 standard; protein; 452 AA.

AC AAY21627;  
 XX  
 DT 11-AUG-1999 (first entry)

DE Ligand binding domain of nuclear receptor hAR.  
 XX  
 KM Thyroid hormone receptor; aromatic compound; ligand binding domain;  
 KM alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride;  
 KM plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH;  
 KM thyroid hormone replacement therapy; nuclear receptor.

OS Homo sapiens.  
 XX  
 PN WO926966-A2.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PR 25-NOV-1998; 98WO-US25296.

XX 26-NOV-1997; 97US-0980115.  
 PR (REGC ) UNIV CALIFORNIA.

XX Apriletti JW, Baxter JD, Fletterick RJ, Kushner PJ;  
 PI Scanlan TS, Shlau AK, Wagner RL, West BL;  
 XX WPI, 1999-357810/30.

XX Modulating activity of a thyroid hormone receptor  
 PT  
 XX Disclosure; Fig 3H-R; 447p; English.

CC The invention relates to a method for modulating activity of a thyroid  
 CC hormone receptor that comprises administration of an aromatic compound  
 CC which fits spatially and preferentially into a thyroid hormone ligand  
 CC binding domain. The aromatic compound (of a specified formula) can be  
 CC used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at  
 CC levels which do not significantly modify cardiac GPDH levels and are  
 CC indicated in the treatment of obesity. The compound also lower total  
 CC plasma cholesterol and triglyceride levels and can be used as anti-  
 CC hypertriglyceridaemic agents. The compound may also be used for treating  
 CC atherosclerosis and may be indicated in thyroid hormone replacement  
 CC therapy in patients with compromised cardiac function. Sequences  
 CC AAY21621-636 amino acid sequences of ligand binding domains of several  
 CC members of the nuclear receptor superfamily.

XX Sequence 452 AA;

Query Match 98.4%; Score 1349.5; DB 20; Length 452;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-132;

\* Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIGYECOPITLVNLEAIBPGVCAAGHNNQDPSFALLSSINELGERQLVHVVKAK 61  
 DB 195 SH-IBGYECOPITLVNLEAIBPGVCAAGHNNQDPSFALLSSINELGERQLVHVVKAK 253  
 QY 62 ALPGFRLNLYVDQDMVIOYQSMGMLVFPAMGWSFTNVNSRMLYFAPDLVFNERYMHSRM 121  
 DB 254 ALPGFRLNLYVDQDMVIOYQSMGMLVFPAMGWSFTNVNSRMLYFAPDLVFNERYMHSRM 313  
 QY 122 YSQCRMHLISOEFGMLQITPQEFCKKALLFSIIPVDGLKNQKFFDELNNYIKELDR 181  
 DB 314 YSQCRMHLISOEFGMLQITPQEFCKKALLFSIIPVDGLKNQKFFDELNNYIKELDR 373  
 QY 182 IIAKCRKNPTSCSRFFYQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEITIS 241  
 DB 374 IIAKCRKNPTSCSRFFYQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEITIS 433  
 QY 242 VQVPKILSGKVPPIYFHTQ 260  
 DB 434 VQVPKILSGKVPPIYFHTQ 452

#### RESULT 4

ID ABG71292 standard; Protein; 839 AA.

XX ABG71292;

DT 08-JAN-2003 (first entry)

XX Human androgen receptor.

XX Pharmacological; receptor; endocrine disrupting chemical; EDC;  
 KW simultaneous determination; ligand binding activity; human;  
 XX androgen receptor.

OS Chimeric - Homo sapiens.

OS Chimeric - Bacteria.  
 OS Synthetic.

PN JP2002243739-A.  
 XX 28-AUG-2002.

XX 21-FEB-2001; 2001JP-0045420.

XX 21-FEB-2001; 2001JP-0045420.

XX (TOWN ) TOYOBO KK.

XX WPI, 2002-744851/81.

DR N-PSDB; ABS56325.

PT A method and a kit for simultaneous determination of binding activity  
 of ligand with 2 or more receptors using their corresponding tracers

XX Example 3; Page 13-15; 22pp; Japanese.

CC The present invention relates to a new method for simultaneous  
 CC determination of binding activity of a ligand with 2 or more receptors  
 CC using their corresponding tracers, and a kit for the determination.  
 CC The invention can be used for screening of ligands with pharmacological  
 CC activity via receptor and endocrine disrupting chemicals (EDCs). The  
 CC invention is advantageous as it allows simultaneous determination of  
 CC binding activity of ligand. The present amino acid sequence represents  
 CC the human androgen receptor as described in the invention.

XX Sequence 839 AA;

Query Match 98.4%; Score 1349.5; DB 23; Length 839;  
 Best Local Similarity 99.6%; Pred. No. 3.6e-132;

\* Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHMIGYECOPITLVNLEAIBPGVCAAGHNNQDPSFALLSSINELGERQLVHVVKAK 61  
 DB 582 SH-IBGYECOPITLVNLEAIBPGVCAAGHNNQDPSFALLSSINELGERQLVHVVKAK 640  
 QY 62 ALPGFRLNLYVDQDMVIOYQSMGMLVFPAMGWSFTNVNSRMLYFAPDLVFNERYMHSRM 121  
 DB 641 ALPGFRLNLYVDQDMVIOYQSMGMLVFPAMGWSFTNVNSRMLYFAPDLVFNERYMHSRM 700  
 QY 122 YSQCRMHLISOEFGMLQITPQEFCKKALLFSIIPVDGLKNQKFFDELNNYIKELDR 181  
 DB 701 YSQCRMHLISOEFGMLQITPQEFCKKALLFSIIPVDGLKNQKFFDELNNYIKELDR 760  
 QY 182 IIAKCRKNPTSCSRFFYQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEITIS 241  
 DB 761 IIAKCRKNPTSCSRFFYQLTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEITIS 820  
 QY 242 VQVPKILSGKVPPIYFHTQ 260  
 DB 821 VQVPKILSGKVPPIYFHTQ 839

#### RESULT 5

ID AAG68238 standard; Protein; 839 AA.

XX AAG68238;

DT 08-FEB-2002 (first entry)

XX Fused androgen receptor (AR) protein SEQ ID NO.11.

XX Human; androgen receptor; AR; fused androgen receptor protein;  
 KW fusion androgen receptor protein; sugar-combining protein;  
 XX maltose-combining protein.

OS Chimeric - Homo sapiens.

OS Chimeric - Unidentified.  
 PN JP2001252080-A.



PD 18-SBP-2001.  
 XX 13-MAR-2000; 2000JP-0069030.  
 XX 13-MAR-2000; 2000JP-0069030.  
 XX (TOWM) TOYOBO KK.  
 XX WPI; 2002-029658/04.  
 DR N-PSDB; ABA01683.  
 XX  
 XX New polypeptide for screening drugs, comprises an androgen receptor  
 PT protein fused with a sugar-combining protein  
 PS Claim 8; Page 11-13; 16pp; Japanese.  
 XX  
 XX The present invention describes a fused androgen receptor (AR) protein  
 CC prepared by fusing an androgen receptor protein with a sugar-combining  
 CC protein. Also described are: (1) a gene encoding the above fused AR  
 CC protein; (2) a vector carrying the above gene; (3) a transformant in  
 CC which the above vector is introduced to a microbe and a gene encoding  
 CC the fused AR protein is expressed; (4) the preparation of a fused AR  
 CC protein in which the above transformant is cultured and the fused AR  
 CC protein is collected from the resultant culture; and (5) a reagent for  
 CC detecting the presence of interaction with a ligand containing the  
 CC above fused AR protein, a solvent for dissolving chemical substances  
 CC and a diluent liquid of the dissolved chemical substances. The fusion  
 CC protein can be used for screening drugs. The present sequence represents  
 CC the AR protein and sugar-combining protein fusion protein from the  
 CC present invention.  
 XX  
 XX  
 SQ Sequence 839 AA;  
 Query Match 98.4%; Score 1349.5; DB 23; Length 839;  
 Best Local Similarity 99.6%; Pred. No. 3.6e-132;  
 Matches 258; Conservative 0; Mismatches- 0; Indels 1; Gaps 1;  
 QY 2 SHMIEGECOPFLNVLTAIEIRGVVCAAGHNNQPSFALLSLNIEGROLVHVYKMAK 61  
 DB 582 SH-IEGECOPFLNVLTAIEIRGVVCAAGHNNQPSFALLSLNIEGROLVHVYKMAK 640  
 QY 62 ALPGFRNLAVDDQMAVIOYSMMGLVFPAMGWRSTFNVSRLMYPAPDLVFNERYMKSRL 121  
 DB 641 ALPGFRNLAVDDQMAVIOYSMMGLVFPAMGWRSTFNVSRLMYPAPDLVFNERYMKSRL 700  
 QY 122 YSQCVMRRLHLSOEFQWLTTPQEFLLCKKALLFSIIIPVDGLKNOKFDELRMNYIKELDR 181  
 DB 701 YSQCVMRRLHLSOEFQWLTTPQEFLLCKKALLFSIIIPVDGLKNOKFDELRMNYIKELDR 760  
 QY 182 IIAKCKRNKPTSCSRFPYQTLKLDVVOPIARELHQPFDLLIKSHNVSVDPPEMAEITIS 241  
 DB 761 IIAKCKRNKPTSCSRFPYQTLKLDVVOPIARELHQPFDLLIKSHNVSVDPPEMAEITIS 820  
 QY 242 VQVPKILSGKVPKPIYFHTQ 260  
 DB 821 VQVPKILSGKVPKPIYFHTQ 839  
 RESULT 6  
 AAE32995  
 ID AAE32995 standard; Protein; 895 AA.  
 XX  
 XX AAE32995;  
 XX  
 XX 02-APR-2003 (first entry)  
 XX  
 XX Macaca mulatta androgen receptor (rhAR).  
 XX  
 XX Androgen receptor; rhAR protein; bone formation; atherosclerosis; acne;  
 KM myoanabolism; sarcopenia; benign prostatic hyperplasia; hypogonadism;  
 KM lipid metabolism; hirsutism; prostate disease; hippocampal function;  
 KM cancer; rhesus monkey; single nucleotide polymorphism; SNP; therapy.  
 XX

OS Macaca mulatta.  
 FH Key Location/Qualifiers  
 FT Misc-difference 210  
 FT /note= "This residue changes to Gly due to single  
 FT nucleotide polymorphism (SNP)"  
 FT Domain 535..600  
 FT /note= "DNA binding domain"  
 PN WO200290529-A1.  
 XX  
 XX 14-NOV-2002.  
 XX  
 XX 03-MAY-2002; 2002WO-US14175.  
 XX  
 XX 08-MAY-2001; 2001US-289573P.  
 XX  
 XX (MERI) MERCK & CO INC.  
 XX  
 XX Towler DA, Chen F;  
 XX WPI; 2003-103516/09.  
 DR N-PSDB; AAD50740.  
 XX  
 XX  
 PT New DNA encoding Macaca mulatta androgen receptor (rhAR) protein,  
 PT useful for screening rhAR agonists and/or antagonists, and in  
 PT identifying tissue selective androgen compounds such as those active in  
 PT bone formation or myoanabolism  
 XX  
 XX Claim 25; Page 38; 84pp; English.  
 XX  
 XX The invention relates to a DNA encoding Macaca mulatta androgen receptor  
 CC (rhAR) protein. Nucleic acid molecules of the invention are useful for  
 CC screening agonists and/or antagonists of rhAR and in identifying tissue  
 CC selective androgen compounds including those active in bone formation,  
 CC myoanabolism, treatment of sarcopenia, benign prostatic hyperplasia,  
 CC acne, hirsutism, male hypogonadism, atherosclerosis, relief of post-  
 CC menopausal symptoms, treatment and prevention of prostate or breast  
 CC cancer and management of lipids. AR modulators may be used to regulate  
 CC development, production and maintenance of bone and muscle, in the  
 CC treatment of prostate disease and in regulation of lipid metabolism  
 CC and hippocampal function. The present sequence is Macaca mulatta  
 CC (rhesus monkey) androgen receptor.  
 XX  
 XX  
 SQ Sequence 895 AA;  
 Query Match 98.4%; Score 1349.5; DB 24; Length 895;  
 Best Local Similarity 99.6%; Pred. No. 3.9e-132;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SHMIEGECOPFLNVLTAIEIRGVVCAAGHNNQPSFALLSLNIEGROLVHVYKMAK 61  
 DB 638 SH-IEGECOPFLNVLTAIEIRGVVCAAGHNNQPSFALLSLNIEGROLVHVYKMAK 696  
 QY 62 ALPGFRNLAVDDQMAVIOYSMMGLVFPAMGWRSTFNVSRLMYPAPDLVFNERYMKSRL 121  
 DB 697 ALPGFRNLAVDDQMAVIOYSMMGLVFPAMGWRSTFNVSRLMYPAPDLVFNERYMKSRL 756  
 QY 122 YSQCVMRRLHLSOEFQWLTTPQEFLLCKKALLFSIIIPVDGLKNOKFDELRMNYIKELDR 181  
 DB 757 YSQCVMRRLHLSOEFQWLTTPQEFLLCKKALLFSIIIPVDGLKNOKFDELRMNYIKELDR 816  
 QY 182 IIAKCKRNKPTSCSRFPYQTLKLDVVOPIARELHQPFDLLIKSHNVSVDPPEMAEITIS 241  
 DB 817 IIAKCKRNKPTSCSRFPYQTLKLDVVOPIARELHQPFDLLIKSHNVSVDPPEMAEITIS 876  
 QY 242 VQVPKILSGKVPKPIYFHTQ 260  
 DB 877 VQVPKILSGKVPKPIYFHTQ 895  
 RESULT 7  
 AAE32996

[illegible]

Db	757	YSGCVRNRHLSQEGWQIIPQELCKALKLLSIIFVDDLNQKQFDELARMYIKELDR	816
Qy	182	IIACKRRNPISCSRRFQLTITLSDSVPIARELHQTFDLLISHWVSVDPEMAEIIIS	241
Db	817	IIACKRRNPISCSRRFQLTITLSDSVPIARELHQTFDLLISHWVSVDPEMAEIIIS	876
Qy	242	VOVKIISGKVKPIYFHTQ	260
Db	877	VOVKIISGKVKPIYFHTQ	895
RESULT 8			
ID	ABP72589	standard; Protein; 899 AA.	
AC	ABP72589;		
XX	29-MAY-2003	(first entry)	
DT	Mouse androgen receptor.		
DE	Androgen receptor; receptor; ARKO; mouse; transgenic mouse;		
KW	knockout animal; cancer; tumour.		
XX	Mus musculus.		
OS	WO2003012394-A2.		
PN	13-FEB-2003.		
PD	29-JUL-2002; 2002WQ-US24234.		
PF	27-JUL-2001; 2001US-308356P.		
PR	17-MAY-2002; 2002US-381309P.		
XX	(UTRP ) UNIV ROCHESTER.		
PA	Chang C, Yeh S;		
XX	WPI; 2003-247910/25.		
DR	N-PSDB; ABZ81677, ABZ81679.		
PT	Composition for generating androgen receptor knockout mice for studying		
PT	the role of an androgen receptor in cancer, comprises a cell having a		
PT	disrupted androgen receptor gene -		
XX	Disclosure; Page 75; 99pp; English.		
PS	The present sequence is that of the murine androgen receptor (AR).		
CC	The invention relates to compositions and methods for disrupting an		
CC	AR gene and for studying the role of the AR in cancer. Compositions		
CC	comprising a cell having a disrupted AR gene are claimed. The cell		
CC	is especially an embryonic stem cell, an embryonic germ cell, a		
CC	breast cell, a breast cancer cell, an ovary cell, an ovary cancer		
CC	cell, a prostate cell, a testis cell, a bone cell, a brain cell, a		
CC	neural cell or a muscle cell. Also claimed is a transgenic mammal,		
CC	especially a mouse, comprising a disrupted AR gene, especially a		
CC	disrupted AR gene lacking exon 2 of the AR gene, where the		
CC	disruption is produced by the action of a cre recombinase under the		
CC	control of an inducible promoter specific for breast, ovary, neural,		
CC	bone, testis, liver or prostate. Also claimed is a method of		
CC	determining the effect of a steroid on the AR by incubating the		
CC	steroid with an AR disrupted cell line and assaying its effect. A		
CC	claimed method of evaluating treatment for cancer xenografts		
CC	involves infecting a cell that has a disrupted AR locus into an		
CC	ovarectomised mouse, especially a nude mouse, where the xenograft		
CC	comprises a cell from a breast cancer or ovarian cancer tissue line.		
CC	Tumour formation can be evaluated in an androgen receptor knockout		
CC	(ARKO) mouse by injecting the cancer-causing agent into the mouse.		
XX	Sequence	899 AA;	

Query Match
98.4%; Score 1349.5; DB 24; Length 899;

Best Local Similarity 99.6%; Pred. No. 4e-132;  
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHNIEGECOPIFLNVLEAIEPGVVCAGHDNNQDPSPALLSSINELGERQLVHYVYKAK 61  
DB 642 SH-1BEGECOPIFLNVLEAIEPGVVCAGHDNNQDPSPALLSSINELGERQLVHYVYKAK 700  
QY 62 ALPGFRNLHVDDQMAVIOYSWGMGLVFPAMGMRSTNVNSRMLYFAPDLVFNERYRMHKSMM 121  
DB 701 ALPGFRNLHVDDQMAVIOYSWGMGLVFPAMGMRSTNVNSRMLYFAPDLVFNERYRMHKSMM 760  
QY 122 YSCQVRMRHLSQERGMLOITPOEFLCMKALLFSIIPVDGLKNOKFPDELRLMNYIKELDR 181  
DB 761 YSCQVRMRHLSQERGMLOITPOEFLCMKALLFSIIPVDGLKNOKFPDELRLMNYIKELDR 820  
QY 182 IIACKRNKPTSCSRPFYQTLKLDVOPVPIARELHOFTEFLLIKSHMVSVDPEEMAAEIIIS 241  
DB 821 IIACKRNKPTSCSRPFYQTLKLDVOPVPIARELHOFTEFLLIKSHMVSVDPEEMAAEIIIS 880  
QY 242 VOVPKILSGKVKPIYFHTQ 260  
DB 881 VOVPKILSGKVKPIYFHTQ 899

## RESULT 9

AAP93110  
ID AAP93110 standard; protein; 902 AA.

AC AAP93110;

DT 25-MAR-2003 (updated)

DT 19-MAR-1990 (first entry)

DE Rat androgen receptor.

KM Rat androgen receptor; monoclonal antibody; polyclonal antibody; cancer.

OS Rattus rattus.

PN W08909791-A.

PD 19-OCT-1989.

PF 13-APR-1989; 89WO-US01548.

PR 14-APR-1988; 88US-0182646.

PA (UYN-C) UNIV OF N CAROLINA.

PI French FS, Wilson EM, Joseph DR, Lubahn DB;

DR WPI; 1989-324206/44.

DR N-PSDB; AAN91773.

PT DNA encoding androgen receptor protein - useful for transforming eukaryotic hosts for protein expression and subsequent antibody prodn.

PS Disclosure; Fig. 5; 41pp; English.

XX Androgen receptor protein (AR) is used to produce mono- or poly-clonal antibodies. These are used for the detection and quantification of AR in the presence of endogenous androgen, as androgen will not interfere with binding. They may be used in assays to determine and quantify cellular distribution of AR in tumour tissue, and are esp. useful for evaluating prostate cancers to determine responsiveness to androgen withdrawal therapy.

CC (Updated on 25-MAR-2003 to correct PA field.)

SO Sequence 902 AA;

Query Match 98.4%; Score 1349.5; DB 10; Length 902;  
Best Local Similarity 99.6%; Pred. No. 4e-132;  
Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SHNIEGECOPIFLNVLEAIEPGVVCAGHDNNQDPSPALLSSINELGERQLVHYVYKAK 61  
DB 645 SH-1BEGECOPIFLNVLEAIEPGVVCAGHDNNQDPSPALLSSINELGERQLVHYVYKAK 703  
QY 62 ALPGFRNLHVDDQMAVIOYSWGMGLVFPAMGMRSTNVNSRMLYFAPDLVFNERYRMHKSMM 121  
DB 704 ALPGFRNLHVDDQMAVIOYSWGMGLVFPAMGMRSTNVNSRMLYFAPDLVFNERYRMHKSMM 763  
QY 122 YSCQVRMRHLSQERGMLOITPOEFLCMKALLFSIIPVDGLKNOKFPDELRLMNYIKELDR 181  
DB 764 YSCQVRMRHLSQERGMLOITPOEFLCMKALLFSIIPVDGLKNOKFPDELRLMNYIKELDR 823  
QY 182 IIACKRNKPTSCSRPFYQTLKLDVOPVPIARELHOFTEFLLIKSHMVSVDPEEMAAEIIIS 241  
DB 824 IIACKRNKPTSCSRPFYQTLKLDVOPVPIARELHOFTEFLLIKSHMVSVDPEEMAAEIIIS 883  
QY 242 VOVPKILSGKVKPIYFHTQ 260  
DB 884 VOVPKILSGKVKPIYFHTQ 902

## RESULT 10

AAP91006  
ID AAP91006 standard; protein; 902 AA.

AC AAP91006;

DT 25-MAR-2003 (updated)

DT 28-FEB-1990 (first entry)

DE Rat androgen receptor DNA clone.

KM Androgen receptor; TR2 polypeptide;

OS Rat.

PN Key Location/Qualifiers

FT Region 1..902

FT /tag= a

FT /product=98 kD polypeptide

FT 170..902

FT /tag= b

FT /product=79 kD polypeptide

PN W08909223-A.

PD 05-OCT-1989.

PF 24-MAR-1989; 89WO-JP01238.

PR 30-MAR-1988; 88US-0176107.

PR 05-OCT-1988; 88US-0253807.

PR 21-FEB-1989; 89US-0312763.

PA (ARCH-) ARCH DEV CORP.

PI Liao S, Chang C;

DR WPI; 1989-309501/42.

DR N-PSDB; AAN91578.

PT New DNA encoding new androgen receptor and TR2 polypeptide(s) - able to bind DNA, and derived antibodies, useful for receptor assay and purification.

PS Claim 8; Fig 3; 60pp; English.

CC The protein is used to raise antibodies for receptor assays and for affinity purification.

CC The 98 kD product starts at the first Met codon; the 79 kD product starts from the second.

CC (Updated on 25-MAR-2003 to correct PF field.)

(Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC XX Sequence 902 AA;  
 Query Match 98.4%; Score 1349.5; DB 10; Length 902;  
 Best Local Similarity 99.6%; Pred. No. 4e-132;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SHMIEGECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSSLNELGSRQLVHVVMK 61  
 DB 645 SH-IEGECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSSLNELGSRQLVHVVMK 703  
 QY 62 ALPGFRLHVDQMAVIOYSWGLMVFAMGMSFTNVNSRLYFAPDLVFNRYRMKSRM 121  
 DB 704 ALPGFRLHVDQMAVIOYSWGLMVFAMGMSFTNVNSRLYFAPDLVFNRYRMKSRM 763  
 QY 122 YSCVVRHLSOERGMLOITPOEFLCMKALLFSIIPVDGLKNQKPFDELRYMYIKELDR 181  
 DB 764 YSCVVRHLSOERGMLOITPOEFLCMKALLFSIIPVDGLKNQKPFDELRYMYIKELDR 823  
 QY 182 IIAKCRKNTSCSRPFYQLTKLDSVOPFARLHQFTFDLLIKSHMVSVDPEEMAEIIS 241  
 DB 824 IIAKCRKNTSCSRPFYQLTKLDSVOPFARLHQFTFDLLIKSHMVSVDPEEMAEIIS 883  
 QY 242 VOVPKILSGKVPKPIYFHTQ 260  
 DB 884 VOVPKILSGKVPKPIYFHTQ 902  
 RESULT 11  
 ABG74229  
 ID ABG74229 standard; Protein; 907 AA.  
 AC ABG74229;  
 DT 16-APR-2003 (first entry)  
 DE Canine Androgen receptor.  
 XX DOG; receptor; androgen receptor; AR; cytostatic; osteopathic;  
 KM neuroleptic; canine disorder; cancer; mood disorder; temper disorder;  
 KM frailty; muscular degeneration; bone loss.  
 OS Canis familiaris.  
 XX US2002161194-A1.  
 PN 31-OCT-2002.  
 PD 09-NOV-2001; 2001US-0008739.  
 PF 09-NOV-2001; 2001US-0008739.  
 PR 09-NOV-2000; 2000US-247373P.  
 PA (CAST/) CASTLEBERRY T A.  
 PA (LUBB/) LU B.  
 PA (OWEN/) OWEN T A.  
 PA (SMOC/) SMOCK S L.  
 PI Castleberry TA, Lu B, Owen TA, Smock SL;  
 DR WPI; 2003-209230/20.  
 DR N-PsDB; ABX16536.  
 XX New isolated canine androgen receptor protein, useful for diagnosing,  
 PT classifying, prognosing and/or treating canine diseases (e.g. cancer)  
 PT and in studying the molecular and biochemical actions of androgens in  
 PT canine bone  
 XX Claim 1; Fig 1; 20pp; English.  
 PS The invention relates to an isolated proteinaceous molecule having canine  
 CC androgen receptor (AR) activity (appearing as ABG74229), optionally

CC having one or more conservative substitutions. Also included are  
 CC an isolated DNA molecule encoding the above proteinaceous molecule,  
 CC a recombinant expression vector comprising the above DNA molecule,  
 CC a cell transformed by the expression vector cited above, producing the  
 CC proteinaceous molecule by culturing the cell cited above, a specific  
 CC binding partner that selectively binds to the proteinaceous molecule,  
 CC discovering ligands for the canine AR protein, and discovering modulators  
 CC of canine AR protein activity. The proteinaceous molecule is useful in  
 CC veterinary purposes for diagnosing, classifying, prognosing and/or  
 CC treating canine disorders (e.g. cancer, mood or temper disorders, and  
 CC frailty associated with muscular degeneration or bone loss) which maybe  
 CC characterised as related to the interaction between a cell receptor and  
 CC biochemical actions of androgens in canine bone. The DNA molecule  
 CC encoding the proteinaceous molecule is used in DNA hybridisation  
 CC processes to locate the canine gene position and/or the position of any  
 CC related gene family in a chromosome map. These may also be used for  
 CC identifying canine gene disorders at the DNA level and used as gene  
 CC markers for identifying neighbouring genes and their disorders.  
 CC The present sequence represents the canine androgen receptor.  
 XX  
 SQ Sequence 907 AA;  
 Query Match 98.4%; Score 1349.5; DB 24; Length 907;  
 Best Local Similarity 99.6%; Pred. No. 4e-132;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SHMIEGECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSSLNELGSRQLVHVVMK 61  
 DB 650 SH-IEGECOPIFLNVLEAIEPGVVCAGHDNNQPSFALLSSLNELGSRQLVHVVMK 708  
 QY 62 ALPGFRLHVDQMAVIOYSWGLMVFAMGMSFTNVNSRLYFAPDLVFNRYRMKSRM 121  
 DB 709 ALPGFRLHVDQMAVIOYSWGLMVFAMGMSFTNVNSRLYFAPDLVFNRYRMKSRM 768  
 QY 122 YSCVVRHLSOERGMLOITPOEFLCMKALLFSIIPVDGLKNQKPFDELRYMYIKELDR 181  
 DB 769 YSCVVRHLSOERGMLOITPOEFLCMKALLFSIIPVDGLKNQKPFDELRYMYIKELDR 828  
 QY 182 IIAKCRKNTSCSRPFYQLTKLDSVOPFARLHQFTFDLLIKSHMVSVDPEEMAEIIS 241  
 DB 829 IIAKCRKNTSCSRPFYQLTKLDSVOPFARLHQFTFDLLIKSHMVSVDPEEMAEIIS 888  
 QY 242 VOVPKILSGKVPKPIYFHTQ 260  
 DB 889 VOVPKILSGKVPKPIYFHTQ 907  
 RESULT 12  
 AAY33491  
 ID AAY33491 standard; Protein; 918 AA.  
 AC AAY33491;  
 DT 19-JAN-2000 (first entry)  
 DE Human androgen receptor protein.  
 XX  
 XX Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;  
 KM huntingtin polypeptide; Machado-Joseph disease; SCAL; SC2; SC6;  
 KM atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;  
 KM Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;  
 KM dentatorubropallidolysian atrophy; cell proliferation; cell survival;  
 KM neoplastic; malignant; autoimmune; fibrotic.  
 XX  
 OS Homo sapiens.  
 XX MO3945944-A1.  
 PN 16-SEP-1999.  
 PD 11-MAR-1999; 99WO-US05250.  
 PP

PR 12-MAR-1998; 98US-0041886.  
 XX (BURN-) BURNHAM INST.  
 PA  
 XX  
 PI Bredesen DE, Rabizadeh S;  
 XX  
 DR MPI, 1999-561617/47.  
 DR N-PSDB; AAZ23424.  
 XX  
 PT New proapoptotic dependence peptides, used to develop products for  
 PT treating, e.g. Alzheimer's disease -  
 XX  
 PS Disclosure; Page 90-93; 1999p; English.  
 XX  
 CC This invention describes novel pure proapoptotic dependence peptides  
 CC which comprise a sequence of an active dependence domain selected from  
 CC dependence polypeptides consisting of p75NTR, androgen receptor, DCC,  
 CC huntingtin polypeptide, Machado-Joseph disease gene product, SCA1, SCA2,  
 CC SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable  
 CC of inducing cell death and can be used to develop products to mediate or  
 CC inhibit apoptosis. The methods can be used for reducing the severity of  
 CC a proapoptotic dependence domain mediated pathological conditions e.g.  
 CC Huntington's disease, Alzheimer's disease, Kennedy's disease,  
 CC Spinocerebellar ataxias, dentatorubropallidoluysian atrophy,  
 CC Machado-Joseph disease, stroke or head trauma. They can also be used for  
 CC reducing the severity of a pathological condition mediated by upregulated  
 CC cell proliferation or cell survival e.g. neoplastic, malignant,  
 CC autoimmune or fibrotic conditions. This sequence represents a human  
 CC androgen receptor described in the method of the invention.  
 XX  
 SQ Sequence 918 AA;  
 1 Query Match 98.4%; Score 1349.5; DB 20; Length 918;  
 1 Best Local Similarity 99.6%; Pred. No. 4.1e-132;  
 1 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 1  
 2 SHMISGECOPIFLNVLAIEIPGVCAGHNNOPDSFALLSLNIEGROLVHVVKMAK 61  
 661 SH-IEGVCOPIFLNVLAIEIPGVCAGHNNOPDSFALLSLNIEGROLVHVVKMAK 719  
 DB  
 QY 62 ALPGFRNLHVDDQMAVIOYSMGLVFPAMGWSFTNVNSRMLYFAPDLVFNEXYRHKSRM 121  
 DB 720 ALPGFRNLHVDDQMAVIOYSMGLVFPAMGWSFTNVNSRMLYFAPDLVFNEXYRHKSRM 779  
 QY 122 YSOCTVRMHLISOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFDELPMNYIKELDR 181  
 DB 780 YSOCTVRMHLISOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFDELPMNYIKELDR 839  
 QY 182 IIACTRRKNTSCSRPFYOLTKLDSVOPIARELHOFTDLLIKSHMVSVPFEMMAEITS 241  
 DB 840 IIACTRRKNTSCSRPFYOLTKLDSVOPIARELHOFTDLLIKSHMVSVPFEMMAEITS 899  
 QY 242 VQVPKILSGKVPPIYFHTQ 260  
 DB 900 VQVPKILSGKVPPIYFHTQ 918  
 DB  
 RESULT 13  
 AAP90996  
 ID AAP90996 standard; protein; 919 AA.  
 AC AAP90996;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 28-FEB-1990 (first entry)  
 XX  
 DE Human androgen receptor DNA clone.  
 XX Androgen receptor; TR2 polypeptide;  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers

FT Region 1..919  
 FT /\*tag= a  
 FT /product=98 kD polypeptide  
 FT Region  
 FT 185..919  
 FT /\*tag= b  
 FT /product=79 kD polypeptide  
 XX  
 PN W08909223-A.  
 XX  
 PD 05-OCT-1989.  
 XX  
 XX 24-MAR-1989; 89WO-JP01238.  
 XX  
 PR 30-MAR-1988; 88US-0176107.  
 PR 05-OCT-1988; 88US-0253807.  
 PR 21-FEB-1989; 89US-0312763.  
 XX  
 PA (ARCH-) ARCH DEV CORP.  
 PI Liao S, Chang C;  
 XX  
 DR MPI; 1989-309501/42.  
 DR N-PSDB; AAN91577.  
 XX  
 PT New DNA encoding new androgen receptor and TR2 polypeptide(s) - able  
 PT to bind DNA, and derived antibodies, useful for receptor assay and  
 PT purification.  
 XX  
 PS Claim 8; Fig 3; 60pp; English.  
 XX  
 CC The protein is used to raise antibodies for receptor assays and for  
 CC affinity purification.  
 CC The 98 kD product starts at the first Met codon; the 79 kD product  
 CC starts from the second.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 919 AA;  
 1 Query Match 98.4%; Score 1349.5; DB 10; Length 919;  
 1 Best Local Similarity 99.6%; Pred. No. 4.1e-132;  
 1 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 1  
 2 SHMISGECOPIFLNVLAIEIPGVCAGHNNOPDSFALLSLNIEGROLVHVVKMAK 61  
 662 SH-IEGVCOPIFLNVLAIEIPGVCAGHNNOPDSFALLSLNIEGROLVHVVKMAK 720  
 DB  
 QY 62 ALPGFRNLHVDDQMAVIOYSMGLVFPAMGWSFTNVNSRMLYFAPDLVFNEXYRHKSRM 121  
 DB 721 ALPGFRNLHVDDQMAVIOYSMGLVFPAMGWSFTNVNSRMLYFAPDLVFNEXYRHKSRM 780  
 QY 122 YSOCTVRMHLISOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFDELPMNYIKELDR 181  
 DB 781 YSOCTVRMHLISOEFGMLQITPOEFLCMKALLFSIIPVDGLKNOKFDELPMNYIKELDR 840  
 QY 182 IIACTRRKNTSCSRPFYOLTKLDSVOPIARELHOFTDLLIKSHMVSVPFEMMAEITS 241  
 DB 841 IIACTRRKNTSCSRPFYOLTKLDSVOPIARELHOFTDLLIKSHMVSVPFEMMAEITS 900  
 QY 242 VQVPKILSGKVPPIYFHTQ 260  
 DB 901 VQVPKILSGKVPPIYFHTQ 919  
 DB  
 RESULT 14  
 AAW14783  
 ID AAW14783 standard; Protein; 919 AA.  
 AC AAW14783;  
 XX  
 DT 22-JUN-1997 (first entry)  
 XX

DE Androgen receptor.  
 XX Androgen receptor; acidic fibroblast growth factor; aFGF;  
 KM antisense; benign prostatic hyperplasia; prostate cancer; therapy.  
 XX Homo sapiens.  
 OS  
 XX MO9711170-A1.  
 PN  
 XX 27-MAR-1997.  
 PD  
 XX 20-SEP-1996; 96MO-US15081.  
 PF  
 XX 20-SEP-1995; 95US-0004018.  
 PR  
 XX (WORC-) WORCESTER FOUND BIOMEDICAL RES.  
 PA  
 XX Zamecnik PA;  
 PI  
 XX WPI; 1997-202879/18.  
 DR N-PSDB; AAT63407.  
 XX  
 XX Oligonucleotide(s) antisense to human androgen receptor and acidic  
 PT RGF genes - used to inhibit gene expression, for the treatment of  
 PT benign prostatic hyperplasia  
 XX  
 XX Disclosure; Page 22-28; 51pp; English.  
 PS  
 XX Human androgen receptor (AAW4783) binds testosterone and, acting  
 CC at the transcriptional level, regulates the growth of normal  
 CC prostatic cells. Antisense oligonucleotides (see also AAT63200,  
 CC AAT63404-05) based on an androgen receptor cDNA clone (see also  
 CC AAT63407) can be used to prevent androgen receptor gene expression,  
 CC thereby inhibiting the growth or survival of prostatic cells for  
 CC the treatment of benign prostatic hyperplasia and prostate cancer.  
 XX  
 XX Sequence 919 AA;  
 SQ  
 Query Match 98.4%; Score 1349.5; DB 18; Length 919;  
 Best Local Similarity 99.6%; Pred. No. 4.1e-132;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SHMIEGYECOPFLNVLEAIEBPGVVCAGHDNNQPSFALLSSINELGERQLVHVVKMAK 61  
 DB 662 SH-IEGYECOPFLNVLEAIEBPGVVCAGHDNNQPSFALLSSINELGERQLVHVVKMAK 720  
 QY 62 ALPGFRNLHVDDQNAVIOYSWGLMVFAMGWSFTVNSRMUYFADLVFNEYRMKSRM 121  
 DB 721 ALPGFRNLHVDDQNAVIOYSWGLMVFAMGWSFTVNSRMUYFADLVFNEYRMKSRM 780  
 QY 122 YSCVVRMHLISOBFGLMOTPOEFLCKKALLFSII PVGDKNOKFPBELRMNYIKEIDR 181  
 DB 781 YSCVVRMHLISOBFGLMOTPOEFLCKKALLFSII PVGDKNOKFPBELRMNYIKEIDR 840  
 QY 182 IIAACKRNPTSCSRFRYQUTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEITIS 241  
 DB 841 IIAACKRNPTSCSRFRYQUTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEITIS 900  
 QY 242 VQVPRILSGKVKPIYFHTQ 260  
 DB 901 VQVPRILSGKVKPIYFHTQ 919  
 RESULT 15  
 AAY78914  
 ID AAY78914 standard; proteoin; 919 AA.  
 XX  
 AC AAY78914;  
 XX  
 XX 23-MAY-2000 (first entry)  
 DT  
 XX Human androgen receptor (AR) amino acid sequence.  
 DE

KM Androgen receptor; AR; androgen-independent activation; inhibitor;  
 KM cancer; benign prostatic hyperplasia; hirsutism; androgenic alopecia;  
 KM acne; breast cancer; Kennedy disease; prostate cancer.  
 XX Homo sapiens.  
 OS  
 XX MO200001813-A2.  
 PN  
 XX 13-JAN-2000.  
 PD  
 XX 30-JUN-1999; 99MO-CA00604.  
 PF  
 XX 30-JUN-1998; 98US-0091871.  
 PR  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA  
 XX Sadar MD, Bruchovsky N, Gout PW, Sinek R, Mawji NR;  
 PI  
 XX WPI; 2000-182113/16.  
 DR  
 XX Novel non-androgen ligand binding peptides for inhibiting  
 PT androgen-independent activation of androgen receptor, used for  
 PT screening compounds and for treatment of androgen-mediated diseases  
 PT such as prostate cancer  
 XX  
 XX Disclosure; Page 7; 32pp; English.  
 PS  
 XX This sequence represents the human androgen receptor (AR) amino acid  
 CC sequence. The invention relates to a fragment of the AR corresponding to  
 CC amino acids 234-391 (see AAY78913). The fragment mediates  
 CC androgen-independent activation of the AR. The androgen receptor acts as  
 CC a transcription factor, regulating the expression of certain  
 CC androgen-responsive genes. Interaction of the AR with the protein kinase  
 CC A signal transduction pathway involves interaction with the androgen  
 CC independent region. The AR fragment and peptides derived from it can be  
 CC used as agents for inhibiting androgen independent activation of the  
 CC androgen receptor, as activation domains, and as a tool for screening  
 CC for compounds which affect androgen-independent activation of the AR.  
 CC The peptides, when used in combination with androgen deprivation,  
 CC effectively limit androgen mediated disease progression. These diseases  
 CC include cancer, benign prostatic hyperplasia, hirsutism, androgenic  
 CC alopecia, acne, breast cancer, Kennedy disease, and especially prostate  
 CC cancer. The peptides and nucleic acids encoding them, are especially used  
 CC for the treatment of androgen-mediated diseases, especially prostate  
 CC tumours in patients deprived of androgen.  
 XX  
 XX Sequence 919 AA;  
 SQ  
 Query Match 98.4%; Score 1349.5; DB 21; Length 919;  
 Best Local Similarity 99.6%; Pred. No. 4.1e-132;  
 Matches 258; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 SHMIEGYECOPFLNVLEAIEBPGVVCAGHDNNQPSFALLSSINELGERQLVHVVKMAK 61  
 DB 662 SH-IEGYECOPFLNVLEAIEBPGVVCAGHDNNQPSFALLSSINELGERQLVHVVKMAK 720  
 QY 62 ALPGFRNLHVDDQNAVIOYSWGLMVFAMGWSFTVNSRMUYFADLVFNEYRMKSRM 121  
 DB 721 ALPGFRNLHVDDQNAVIOYSWGLMVFAMGWSFTVNSRMUYFADLVFNEYRMKSRM 780  
 QY 122 YSCVVRMHLISOBFGLMOTPOEFLCKKALLFSII PVGDKNOKFPBELRMNYIKEIDR 181  
 DB 781 YSCVVRMHLISOBFGLMOTPOEFLCKKALLFSII PVGDKNOKFPBELRMNYIKEIDR 840  
 QY 182 IIAACKRNPTSCSRFRYQUTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEITIS 241  
 DB 841 IIAACKRNPTSCSRFRYQUTKLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEITIS 900  
 QY 242 VQVPRILSGKVKPIYFHTQ 260  
 DB 901 VQVPRILSGKVKPIYFHTQ 919

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